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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

December 30, 2005, 18:55:16; Search time 190 Seconds (without alignments) 55.182 Million cell updates/sec Run on:

US-09-914-454B-1 20 Title: Perfect score:

1 tecatgaegtteetgaegtt 20 Sequence:

IDENTITY NUC Scoring table:

4172979 segs, 262114271 residues Searched:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Published Applications NA New:*

1: /cgn2 6/ptodata/1/pubpna/USOB NEW PUB.seq:*
2: /cgn2 6/ptodata/1/pubpna/USOB NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USOT NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USOT NEW PUB.seq:*
5: /cgn2 6/ptodata/1/pubpna/USIO NEW PUB.seq:*
6: /cgn2 6/ptodata/1/pubpna/USIO NEW PUB.seq:*
7: /cgn2 6/ptodata/1/pubpna/USIO NEW PUB.seq:*
8: /cgn2 6/ptodata/1/pubpna/USII NEW PUB.seq:*
9: /cgn2 6/ptodata/1/pubpna/USII NEW PUB.seq:*
9: /cgn2 6/ptodata/1/pubpna/USII NEW PUB.seq:*
10: /cgn2 6/ptodata/1/pubpna/USII NEW PUB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	. Appl	Appl	Appli	Appli	Appl	. Appl	O. App	5. App	6, App	292. App		Ä	Appl	Appl	Appl	Appl	221, App	-	Appl.	Appl	3. App	. ~
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Segmence	Sequence	Sequence
QI	US-10-469-561-5	US-10-619-279-10	US-10-435-656-10	JS-11-025-858-3	US-11-025-858-7	US-11-127-654-63	US-11-127-654-82	US-11-127-654-130	US-11-127-654-145	US-11-127-654-146	US-11-127-654-292 ·	US-11-127-654-916	US-11-154-324-1	JS-11-089-426-22	JS-11-134-918-10	US-11-031-460-10	US-11-087-177-45	US-11-127-654-221	JS-10-750-185-47485	JS-10-497-591A-37	JS-10-497-591A-38	JS-11-127-654-303	JS-10-619-279-70
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& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	92.0	92.0	90.0	90.0	90.0	85.0
Score	20	20	20	20	20	20	20	20	20	20	50	20	20	20	20	20	20	18.4	18.4	18	18	18	17
Result No.		7	٣	4	ß	9	7	c o	6	10	11	12	13	14	15	16	17	18	c 19	20	21	22	23

Sequence 66, Appl Sequence 12, Appl Sequence 7, Appl Sequence 73, Appl Sequence 73, Appl Sequence 74, Appl Sequence 15, Appl Sequence 16, Appl Sequence 11, Appl Sequence 11, Appl Sequence 219, Appl Sequence 219, Appl Sequence 229, Appl Sequence 269, Appl Sequence 779, Appl Sequence 779, Appl Appl Sequence 779, Appl Appl Sequence 779, Appl Appl Sequence 779, Appl Sequence
US-11-127-654-66 US-10-497-591A-12 US-10-619-279-7 US-10-619-279-7 US-10-619-279-7 US-10-435-656-7 US-10-435-656-7 US-10-435-656-7 US-10-435-656-7 US-10-435-656-7 US-11-025-858-2 US-11-025-858-2 US-11-127-654-11 US-11-127-654-11 US-11-127-654-219 US-11-127-654-219 US-11-127-654-268 US-11-127-654-268 US-11-127-654-268 US-11-127-654-268 US-11-127-654-268 US-11-127-654-268 US-11-127-654-268 US-11-127-654-268 US-11-127-654-269 US-11-127-654-269 US-11-127-654-269
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ALIGNMENTS

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules FILE REFERENCE: C1039/7023/HCL
CURRENT APPLICATION NUMBER: US/10/619,279
CURRENT PILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR PILING DATE: 1997-10-30
PRIOR PILING DATE: 1996-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels
           SQUENCE 5. APPLICATION US/10469561

Publication No. US20050260216A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Claire Ashman

APPLICANT: James Scott Crowe
APPLICANT: Jonathan Henry Bliss
TITLE OF INVENTION: VACCINE
FILE REFERENCE: P64355USW

FILE REFERENCE: P64355USW
CURRENT APPLICATION NUMBER: US/10/469,561

CURRENT APPLICATION NUMBER: US/10/469,561

CURRENT PILLING DATE: 203-08-29

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PSSESSE for Windows Version 4.0

SSOFTWARE:
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"Sequence 10, Application US/10619279
"Publication No. US20050267057A1
; GENERAL INFORMATION:
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US-10-469-561-5
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RESULT 5
US-11-025-858-7
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Squence 3, Application US/11025858
Squence 3, Application No. US20050250723A1
GENERAL INFORWATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pascolo, Steve
APPLICANT: Pascolo, Steve
TITLE OF INVENTION: Immunstimulation by chemically modified RNA
FILE REPRENCE: Curevac GmbH (2793-1-002)
CURRENT APPLICATION NUMBER: US/11/025,858
CURRENT FILING DATE: 2004-12-28
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APPLICANT: Kline, Joel N.
APPLICANT: Kline, Joel N.
APPLICANT: Kline, Joel N.
APPLICANT: Klinman, Dennied
APPLICANT: Klinman, Dennied
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
CURRENT APPLICATION NUMBER: US/10/435,656
PRIOR FILING DATE: 1994-07-10
PRIOR FILING DATE: 1995-02-07
PRIOR PILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PASESEQ for Windows Version 3.0
IENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 6; Length 20; 100.0%; Pred: No. 0.27;
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Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                         CTHER INFORMATION: Synthetic Oligonucleotide US-10-619-279-10
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-435-656-10
Sequence 10, Application US/10435656
Publication No. US20050277604A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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hes 20; Conservative
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                                                                                                                                                                                     TYPE: DNA
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Sequence 63, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: INFLAMMATORY DISEASES
TITLE OF INVENTION: INFLAMMATORY DISEASES
TITLE REFERENCE: C1039.70060US01
CURRENT FILING DATE: 2005-05-12
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR PILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
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; Bequence 7, Application US/11025858
; Publication No. US20050250723A1
; GENERAL INFORMATION:
    APPLICANT: Hoerr, Ingmar
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Stew Mulbe, Florian
papelicant: Pascolo, Stew Mulbe, Florian
rithe Represence: Curevac GmbH (2793-1-002)
; FILE REPRESENCE: Curevac GmbH (2793-1-002)
; FRIOR PRICATION NUMBER: US/11/025,858
; PRIOR PILING DATE: 2003-07-03
; PRIOR FILING DATE: 2002-07-03
; PRIOR FILING DATE: 2002-07-03
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 7
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 65.0%; Pred. No. 0.27;
Matches 13; Conservative 7; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: SYNTHETIC Oligonucleotide, CpG RNA 1826
US-11-025-858-3
PRIOR APPLICATION NUMBER: PCT/EP2003/007175
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: DE 10229872.6
PRIOR FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 8
SOFTWARR: Patentin version 3.3
SEQ ID NO 3
LENGTH: 20
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                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
LENGTH: 20
CURRENT APPLICATION NUMBER: US/11/127,654
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PRIOR APPLICATION NUMBER: US 10/112,653
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ORGANISM: Artificial sequence
PEATURE:
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Best Local Similarity
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LENGTH: 20
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| Sequence 82, Application US/11127654
| Sequence 82, Application US/11127654
| Sequence 82, Application NO: US20050250726A1
| GENERAL INPORMATION:
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Regery, Arthur M. |
| TITLE OF INVENTION: INPLANMATORY DISEASES |
| TITLE OF INVENTION: INFLANMATORY DISEASES |
| TITLE OF INVENTION: UNMER: US/11/127,654
| CURRENT APPLICATION NUMBER: US/11/127,654
| CURRENT FILING DATE: 2005-05-12 |
| PRIOR APPLICATION NUMBER: US 60/279,642 |
| PRIOR FILING DATE: 2001-03-29 |
| PRIOR FILING DATE: 2001-03-29 |
| PRIOR FILING DATE: 2001-03-29 |
| SOFTWARE: PatentIn version 3.2 |
| SEQ ID NO 82 |
| LENGTH: 20 |
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APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REPERENCE: C1039.70060US01
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US-11-127-654-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
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Publication No. US20050250726A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCCATGACGTTCCTGACGTT 20
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1 Similarity 100.0%;
20; Conservative 0
              NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
SEQ ID NO 63
LENGTH: 20
                                                                                                                                                                                   ORGANISM: Artificial sequence
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; LOCATION: (17)...(17)
; OTHER INFORMATION: m5c
US-11-127-654-82
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NAME/KEY: modified base
LOCATION: (8)..(8)
OTHER INFORWATION: m5c
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Best Local Similarity
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US-11-127-654-130
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Sequence 145, Application US/11127654

Publication No. US20050250726A1

GENUREAL INPORMATION:

APPLICANT: Krieg, Arthur M.

TITLE OF INVENTION: INPLAMMATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

TITLE OF INVENTION: INPLAMMATORY DISEASES

FILE REPERRACE: C1039,70060US01

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT FILING DATE: 2002-05-12

FRIOR APPLICATION NUMBER: US 00/112,653

FRIOR FILING DATE: 2002-03-29

FRIOR FILING DATE: 2001-03-29

FRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SOFTWARE: Patentin version 3.2
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Sequence 146, Application US/11127654

Publication No. US20050250726A1

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: INFLAMMATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: INFLAMMATORY DISEASES

FILE REFERENCE: C1039-7006001501

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT FILING DATE: 2005-05-12
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                                                                                 Query Match 100.0%; Score 20; DB 7; Length 20; Best Local Similarity 100.0%; Pred. No. 0.27; Matches 20; Conservative 0; Mismatches 0; Indels
; OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-145
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1 rccardacGrrccrGACGTT 20
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               SOFTWARE: Patentin version 3.2
SEQ ID NO 916
LENGTH: 20
                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
NUMBER OF SEQ ID NOS: 1040
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Best Local Similarity
Matches 20; Conserv
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US-11-154-324-1
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Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Breg, Daniel J.
APPLICANT: Breg, Daniel J.
APPLICANT: Breg, Daniel J.
APPLICANT: Breg, Daniel J.
APPLICANTON: INFLAMMATORY DISEASES
TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFRERENCE: C1039.70060US01.
CURRENT APPLICATION NUMBER: US/11/12,654
CURRENT FILING DATE: 2005-05-12
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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GENERAL INCOMAILUR.

APPLICANT: Krieg, Arthur M.

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLBIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMMUNOSTIMULATORY DISEASES

FILE REFERENCE: C1039.70060US01

CURRENT APPLICATION NUMBER: US 10/112,653

PRIOR FILING DATE: 2005-03-19

PRIOR FILING DATE: 2005-03-29

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SOFTWARE: Pacentin version 3.2

SEQ ID NO 292

LENGTH: 20
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                                                                                                                                                                                                                            , OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-146
             PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
SEQ ID NO 146
LENGTH: 20
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Publication No. US20050250726A1
GENERAL INFORMATION:
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US-11-127-654-916
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US-11-127-654-292
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Sequence 22, Application US/11089426
; Bublication No. US2005026122941
; Publication No. US2005026122941
; Publication No. US2005026122941
; Publication No. US2005026122941
; APPLICANT: Gillies, Stephen D. APPLICANT: Gillies, Stephen D. APPLICANT: Wesolowski, John
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILLE REFERENCE: LEX.-007
; CURRENT FILLING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR PILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 20
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                                                                               ch 100.0%; Score 20; DB 7; Length 20; 1 Similarity 100.0%; Pred. No. 0.27; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/11154324

Publication No. US20050255124A1

GENERAL INFORMATION:
APPLICANT: HUGGHTON, Michael
APPLICANT: COATES, Steve
APPLICANT: COATES, Steve
APPLICANT: O'HAGAN, Derek
TITLE OF INVENTION: HCV EIEZ VACCINE COMPOSITIONS
FILE REFERENCE: 2302-17206
CURRENT APPLICATION NUMBER: US/11/154,324
CURRENT FILING DATE: 2005-06-16
PRIOR APPLICATION NUMBER: US/10/187,257
PRIOR PILING DATE: 2002-06-28
NUMBER: OSEQ ID NOS: 5
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 1
LENGTH: 20
; OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-916
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SEQ ID NO 45
LENGTH: 20
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:oligodeoxynucleotide that may be used as
US-11-089-426-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALIDE, JOEN N.
APPLICANT: Kline, Joen N.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
APPLICANT: Steinberg, Alfred D.
TILE REPERENCE: C1039/7048 (AWS)
CURRENT APPLICANTON: Immunostimulatory Nucleic Acid Molecules
FILE REPERENCE: C1039/7048 (AWS)
CURRENT APPLICATION NUMBER: US/11/134,918
PRIOR PILING DATE: 2005-05-05-05
PRIOR PELING DATE: 2001-03-07
PRIOR PLING DATE: 1094-07-15
PRIOR PLING DATE: 1994-07-15
PRIOR PLING DATE: 1995-02-07
PRIOR PLING DATE: 1995-02-07
PRIOR PLING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARR: PartSEQ for Windows Version 3.0
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APPLICANT: Krieg, Arthur M.
APPLICANT: Klime, Joel N.
APPLICANT: Klimman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REPERENCE: C1039/7048 (AMS)
CURRENT APPLICATION NUMBER: US/11/031,460
CURRENT PILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: US/09/818,918
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US/09/818,918
                                                                                                                                                                    100.0%; Score 20; DB 7; Length 20; 100.0%; Pred. No. 0.27; cive 0; Mismatches 0; Indels
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100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels
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Publication No. US20050267064A1
GENERAL INFORMATION:
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Publication No. US20050277609A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-11-134-918-10
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Sequence 221, Application US/11127654
Publication No. U82005025072641
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC;
TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
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Sequence 45, Application US/11087177

Publication No. US20050276756A1

GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
ITILE OF INVENTION: COMPOSITIONS AS ADJUVANTS TO IMPROVE
ITILE OF INVENTION: IMMUNE RESPONSES TO VACCINES AND METHODS OF USE
ITILE OF INVENTION: UMMER: US/11/087,177

CURRENT APPLICATION NUMBER: US/11/087,177

CURRENT PILING DATE: 2004-03-24

PRIOR FILING DATE: 2004-06-23

NUMBER OF SEQ ID NOS: 45

SOOFTHAND OF SEQ ID NOS: 45

SOOFTHAND OF SEQ ID NOS: 45
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Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Synthetic oligonucleotide US-11-031-460-10
PRIOR FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 20
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; OTHER INFORMATION: phosphorothiated bases
US-11-087-177-45
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                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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; Sequence 38, Application US/10497591A
; GENERAL INFORMATION:
APPLICANT: SCHELLACK, CAROLA
; APPLICANT: SCHELLACK, CAROLA
; APPLICANT: EGYED, ALENA
APPLICANT: LINGRAU, KAREN
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGODEOXYNUCLEOTIDES
; TITLE REPERENCE: SONN: 04508
; CURRENT APPLICATION NUMBER: US/10/497,591A
; CURRENT FILING DATE: 2004-06-03
; PRIOR PILING DATE: 2002-12-05
; PRIOR PILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PATCHIN OFF: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 18; DB 6; Length 20; 90.0%; Pred. No. 2.8; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 6; Length 20;
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified base

| LOCATION: (9)..(18)

| OTHER INFORMATION: n = inosine or uracil

US-10-497-591A-38
                                                                                                                                                                                                                                                                     ; NAME/KEY: modified base; i.OCATION: (9)..(18); OTHER INFORMATION: n = inosine or uracil US-10-497-591A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 303, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: A 1924/2001
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 113
SQPTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                      90.08;
                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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US-11-127-654-303
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LENGTH: 20
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; Sequence 47485, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
APPLICANT: MERR, Richard
APPLICANT: ROSENFERD, David
APPLICANT: ROSENFERD, David
APPLICANT: PATEN, Tom
APPLICANT: PATEN, Tom
APPLICANT: PATEN, Dennis
TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLO0-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 47485
LENGTH. 1191
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Sequence 37, Application US/10497591A

Sequence 37, Application No. US20050250716A1

GENERAL INPORMATION:
APPLICANT: SCHULDY, WALTER
APPLICANT: SCHULDY, CAROLA
APPLICANT: LINGNAU, KAREN
TITLE OF INVENTION: INMUNOSTIMULATORY OLIGODEOXYNUCLEOTIDES
FILE REFERENCE: SOUN:045US
CURRENT APPLICATION NUMBER: US/10/497,591A

CURRENT FILING DATE: 2004-06-03
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92.0%; Score 18.4; DB 6; Length 1191;
Best Local Similarity 95.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 1; Indels 0;
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Pred. No. 1.8;
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95.0%; Pred. No. ...
0; Mismatches
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, OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-221
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                          CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: PATENTIN VETBION 3.2
SOFTWARE: 2001-03-29
SEQ ID NO 221
LENGTH: 20
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; ORGANISM: Bovine 19866881256760
US-10-750-185-47485
                                                                                                                                                                                                 LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 95.09
Matches 19; Conservative
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APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMMUNOSTIMULATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/12,653
PRIOR APPLICATION NUMBER: US 60/219,642
PRIOR PILLING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PILLING DATE: 2001-03-29
SURGENT FILING DATE: 2001-03-39
SUPPLICATION NUMBER: 2001-03-39
SUPPLICATION NUMBER: 2001-03-29
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| Sequence 12, Application US/10497591A
| Publication No. US20050250716A1
| GENERAL INFORMATION:
| APPLICANT: SCHMIDT, WALTER
| APPLICANT: SCHMIDT, WALTER
| APPLICANT: BGYED, ALENA
| APPLICANT: INGNAU, KARN
| TITLE OF INVENTION: IMMUNSTIMULATORY OLIGODEOXYNUCLEOTIDES
| TITLE OF INVENTION: IMMUNSTIMULATORY OLIGODEOXYNUCLEOTIDES
| TILE REFERENCE: SONN: 045US
| TILE OF INVENTION: IMMUNST: 2004-06-03
| PRIOR PAPLICATION NUMBER: BCT/EP02/13791
| PRIOR PLING DATE: 2004-06-03
| PRIOR PLING DATE: 2001-12-07
| NUMBER OF SEQ ID NOS: 113
| SEQ ID NO 12
| LENGTH: 20
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8.8;
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                                                                                                                                           Sequence 66, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
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Best Local Similarity 90.0
Matches 18; Conservative
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APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMINOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMMINOSTIMULATORY DISEASES
FILE REPERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 60/219,642
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
LENGTH: 20
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Sequence 70, Application US/10619279

Publication No. US2005267057A1

GENERAL INFORMATION:

HER REPLICATION:

CURRENT PRILING DATE:

CURRENT PILING DATE: 1097-104

PRIOR PPLICATION NUMBER: US/10/619,279

CURRENT FILING DATE: 1997-10-30

PRIOR PPLICATION NUMBER: US 08/960,774

PRIOR PILING DATE: 1997-10-30

PRIOR PILING DATE: 1997-10-30

PRIOR PLING DATE: 1997-10-30

PRIOR PILING DATE: 1997-10-30

PRIOR PLING DATE: 1997-10-30

PRIOR PLING DATE: 1997-10-30

PRIOR PLING DATE: 1995-10-30

PRIOR PLING DATE: 1995-10-30

PRIOR PLING DATE: 1995-10-30

PRIOR PLING DATE: 1995-10-30

SPRIOR PLING DATE: 1995-10-30
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Pred. No. 2.8;
0; Mismatches 2; Indels
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85.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 17; Conservative 0; Mismatches 0; Indels
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il Similarity 90.0%;
18; Conservative
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ORGANISM: Artificial Sequence
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NAME/KEY: misc feature
LOCATION: (17)...(17)
COTHER INPORMATION: I
US-11-127-654-303
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NAME/KEY: misc feature
LOCATION: (8)..(8)
OTHER INFORMATION: I
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Best Local Similarity
Matches 18; Conserva
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Publication No. US20050267057A1
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US-10-435-656-7
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APPLICANT: Krieg, Arthur M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7023/HCL.

FILE REFERENCE: C1039/7023/HCL.

CURRENT PILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: US 08/956,774

PRIOR APPLICATION NUMBER: US 08/738,652

PRIOR PILING DATE: 1996-10-30

PRIOR FILING DATE: 1996-10-30

PRIOR FILING DATE: 1995-02-10-30

PRIOR FILING DATE: 1994-07-15

PRIOR FILING DATE: 1994-07-15

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FASELSEQ for Windows Version 3.0

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide US-10-469-561-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 84.0%; Score 16.8; DB 6; Length 20; Best Local Similarity 90.0%; Pred. No. 11; Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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Pred. No. 11;
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                                                                                                                                      JOSTICATOR OF APPLICATION US/10469561
; Sequence 9, Application US/10469561
; BADDICATION NO. US20050260216A1
GENERAL INFORMATION:
APPLICANT: Claire Abman
; APPLICANT: James Scott Crowe
APPLICANT: Jonathan Henry Ellis
APPLICANT: Jonathan Henry Ellis
APPLICANT: Alan Peter Lewis
TITLE OP INVENTION: VACCINE
FILE REPERENCE: PG4355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT PFLING DATE: 2003-08-29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9; SEQ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.0%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: unknown
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US-10-619-279-7
                                                                                                    RESULT 26
US-10-469-561-9
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; Sequence 7, Application US/10435656
; Publication No. US20050277604A1
; GENERAL INFORMATION:
    APPLICANT: Krieg, Arthur M.
    APPLICANT: Kline, Joel N.
    APPLICANT: Kline, Joel N.
    APPLICANT: Rinman. Dennis
    APPLICANT: Steinberg, Alfred D.
    TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
    TITLE OF INVENTION: IMMUNER: US/10/435,656
    CURRENT FILING DATE: 2003-05-09
    PRIOR FILING DATE: 1994-07-15
    PRIOR FILING DATE: 1995-02-07
    PRIOR PILING DATE: 1996-10-30
    NUMBER OF SEQ ID NOS: 56
    NUMBER OF SEQ ID NOS: 56
    SOFTWARE: FastSEQ for Windows Version 3.0
    LENGTH: 20
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7023/HCL.
FILE REFERENCE: 2003-07-14
FRIOR APPLICATION NUMBER: US/960,774
FRIOR APPLICATION NUMBER: US/98/06,774
FRIOR APPLICATION NUMBER: US/98/738,652
FRIOR APPLICATION NUMBER: US/98/386,063
FRIOR FILING DATE: 1996-10-30
FRIOR FILING DATE: 1996-10-30
FRIOR FILING DATE: 1994-07-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-619-279-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.8;
Pred. No. 11
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Best Local Similarity 90.0%;
Matches 18; Conservative (
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ORGANISM: Artificial Sequence
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RESULT 30

RESULT 28 US-10-619-279-73 ; Sequence 73, Application US/10619279

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Sequence 35

Sequence 35

Sequence 35

Sequence 35

Sequence 35

Septication No. US200502776041

SEREAL INFORMATION:

APPLICANT: Kine, Joel N.

APPLICANT: Kine, Joel N.

APPLICANT: Kinman, Dennis

APPLICANT: Steinberg, Alfred D.

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

FILE REFERENCE: C1039/7048 (AMS)

CURRENT APPLICATION NUMBER: US/10/435,656

CURRENT APPLICATION NUMBER: US 08/276,358

PRIOR FILING DATE: 1994-07-15

PRIOR FILING DATE: 1994-07-15

PRIOR PILING DATE: 1995-02-07

FRIOR FILING DATE: 1996-10-30

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 35

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.0%; Score 16.8; DB 6; Length 20; Best Local Similarity 90.0%; Pred. No. 11; Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-35
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Search completed: December 30, 2005, 20:18:29 Job time : 191 Becs

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OM protein - protein search, using sw model
Run on: December 30, 2005, 08:25:13; Search time 8 Seconds
(without alignments)
412.820 Million cell updates/sec
Title: 2340
Sequence: 1 MKKYLFRAALYGIAAAILAA......KTTGYVWQLIPNGMKPEYRP 441
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 57103 seqs, 7488799 residues
Total number of hits satisfying chosen parameters: 57103
Minimum DB seq length: 0
Maximum Match 000
Post-processing: Minimum Match 1000
Post-processing: Minimum Match 1000
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2: //Ggn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
3: //Ggn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
5: //Ggn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
5: //Ggn2_6/ptodata/1/pubpaa/US01 NEW PUB.pep:*
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7: //Ggn2_6/ptodata/1/pubpaa/US01 NEW PUB.pep:*
8: //Ggn2_6/ptodata/1/pubpaa/US01 NEW PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUPPRIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	2257	96.5	468	9	US-10-467-657-776	Sequence 776, App
7	94	4.0	503	9	US-10-793-626-1810	
٣	94	4.0	576	9	US-10-512-184-65	
4	94	4.0	625	9	US-10-512-184-47	Sequence 47, Appl
īV	92	3.9	473	ø	US-10-467-657-8108	Sequence 8108, Ap
9	90.5	3.9	1389	9	US-10-467-657-334	
7	89.5	3.8	7102	7	US-11-143-980-48	Sequence 48, Appl
80	98	3.7	1572	9	US-10-793-626-2906	2906
σ	82	3.6	808	7	US-11-110-082-38	
2	83.5	3.6	331	9	US-10-878-556A-45	45,
#	83.5	3.6	569	ø	US-10-512-184-66	.99
12	83.5	3.6	618	9	US-10-512-184-48	
13	83	3.5	910	9	US-10-131-826A-112	112,
14	81.5	3.5	409	7	US-11-055-822-290	290
15	81	3.5	534	7	US-11-082-389-348	348,
16	81	3.5	607	7	US-11-096-051-14	14,
17	81	3.5	2376	7	US-11-096-051-4	4,
18	81	3.5	2715	7	US-11-096-051-2	7
13	81	3.5	2715	7	US-11-113-424-51	21,
70	81	3.5	2721	7	US-11-096-051-10	10,
21	81	3.5	2725	7	US-11-096-051-8	8,
22	79.5	3.4	1565	9	US-10-467-657-2704	
23	78	3.3	392	9	US-10-467-657-1784	Sequence 1784, Ap
24	78	3.3	520	9	US-10-131-826A-144	144, A
25	78	3.3	1394	9	US-10-467-657-7930	7930

240

DGKAPILGYAEDPVELFPMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL 300

241

8 8 8 8 8

208 LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL 267

Sequence 47, Appl Sequence 274, Ap Sequence 105, Ap Sequence 586, Appl Sequence 37, Appl Sequence 1632, Appl Sequence 53, Appl Sequence 53, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 55, Appl Sequence 55, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 210, Appl Sequence 210, Appl Sequence 210, Appl Sequence 210, Appl Sequence 2110, Appl Sequence 2111, Appl Sequence 2111	NCLBIC ACIDS	96.5%; Score 2257; DB 6; Length 468; Imilarity 95.7%; Pred. No. 2.3e-190; Conservative 9; Mismatches 10; Indels 0; Gaps 0; MKKYLFRALYGIAAALACQSKSIQTFPOPDTSVINGPDRPVGIPDBAGTTVGGGGAV 60 MKKHLRSALYGIAAALACQSKSIQTFPOPDTSVINGPDRPGIPDBAGTTVGGGGAV 87 YTVVPHLSLPHWAQOPAKSLQSFRLGCANLKOROGOPOVCAQAFOTPVHSFQAKPFER 120 YTVVPHLSNPHWAQDFAKSLQSFRLGCANLKOROGOPOVCAQAFOTPVHSFQAKRFFER 147 YFFPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARPIYGIPDDFISVPLPAGLRSGKA 180 YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARPIYGIPDDFISVPLPAGLRSGKA 180 YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTERARFPIYGIPDDFISVPLPAGLRSGKA 180
0.05-11-143-980-47 6 US-10-858-730-104 6 US-10-858-730-105 6 US-10-821-234-1262 6 US-10-467-657-5866 6 US-10-11-13-826-68 7 US-11-13-826-68 7 US-11-13-825-1632 6 US-10-793-626-1632 6 US-10-793-626-1632 7 US-11-115-639-53 7 US-11-115-639-54 7 US-11-115-639-55	ALIO467657 AL PROTE US/10/46' B=11.04 1.04	.5%; Score 2257; DI .7%; Pred. No. 2.3e e 9; Mismatches AAILAACQSKSIQTFPQPDT; AAILAACQSRSIQTPPQPDT; QPFAKSLQSFRLGCANLKNR(QPFAKSLQSFRLGCANLKNR(GTVTGYYEPVLKGDBRTAQQ
77.5 3.3 5712 77.5 3.3 400 77.5 3.3 529 77.5 3.3 2657 76.5 3.3 745 76.5 3.3 745 76.5 3.3 745 76.3 3.2 1006 76.3 3.2 10	US200502605 US200502605 TION: TION: TANA MATIA F TANA MATIA F TANA MATIA F TANA MATIA F TANA MATIA F TANA MATIA F TANA MATIA F TON NUMBER: TON NUMBER: TON NUMBER: TON NUMBER: TON NUMBER: TON S: 9218 TON OS: 9218 TON OS: 9218	KO (N
22 22 22 22 22 22 22 22 22 22 22 22 22	RESULT 1 US-10-467-657-776 Sequence 776, Applic Publication No. US20 GENERAL INPORMATION: APPLICANT: CHIRON S APPLICANT: PONTANA APPLICANT: PONTANA APPLICANT: PONTANA TITLE OF INVERNY PREFERENCE: TITLE OF INVENTION: FILE REFERENCE: CURRENT FILING DATE: PRIOR APPLICATION N SOFTWARE: SEQMINS9, SEQ ID NO 776 LENGTH: 468 LENGTH: A68 LENGTH: A68 LENGTH: A68 LENGTH: A68 LENGTH: PRI US-10-467-657-776	Query Match Best Local Matches 42: Qy 1 Db 28 Qy 61 Db 88 Qy 121 Db 148

Tue Jan

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APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REPERENCE: 3581.010501
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEG ID NO 65
LENGTH: 576
TYPE: PRT
COGNINSM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT PILING DATE: 2004-10-22
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OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: Gration protein comprising chitinase - linker
OTHER INFORMATION: scrv CWPD2.
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4.0%; Score 94; DB 6; Length 576;
Best Local Similarity 19.8%; Pred. No. 1;
Matches 102; Conservative 50; Mismatches 156; Indels 206;
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US-10-467-657-334
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4.0%; Score 94; DB 6; Length 625;
Best Local Similarity 19.8%; Pred. No. 1.2;
Matches 102; Conservative 50; Mismatches 156; Indels 206; Gaps
                                                                                                      PRATURE: OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: comprising the leader peptide - chitinase - linker OTHER INFORMATION: - scFv CWPD2 - cmyc/His6.
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIKON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONOGOCCAL PROTEINS AND NUCLEIC ACIDS
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 8108
LENGTH: 473
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                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 47
LENGTH: 625
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-----GEYSIEIDPRKVSRDTVLMLGRLGFNRM 183
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                                                                                                                                                                                                               3.9%; Score 92; DB 6; Length 473; llarity 20.7%; Pred. No. 1.2; Conservative 42; Mismatches 90; Indels
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MAIGHANI Vega
APPLICANT: MAIGHANI Vega
TILLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TILLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TILLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PLING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches 179;
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Publication No. US20050260581A1
GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8108
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SOFTWARES SeqWin99, version 1.04
SEQ ID NO 334
LENGTH: 1389
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Matches 106; Conservative
                                                                                                                                                                   Query Match
Best Local Similarity
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1081 VNKVKDIGGKÅRDIGGTTFDKAKDIGTKALDKAKDVSSTVIKGIGDVFDVV----GHPM 1135
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                                                                                                                      Sequence 2906, Application US/10793626
Publication No. US20050255478a1
GENERAL INPORMATION:
APPLICANT: KINMERLY, WILLIAM JOHN
ITILE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2004-03-04
PRIOR PELICATION NUMBER: 60/164,258
PRIOR PLILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE PATENTION VOY. 2.1
SEQ ID NO 2906
ILENGTH: 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 PAGTTVGGGGAVYTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 1572;
21;
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Publication No. US20050266558A1
GENERAL INPORMATION:
APPLICANT: Hall, Claire
APPLICANT: Norriss, Michael Geoffrey
APPLICANT: Saulabury, Keith Martin
TILE OF INVENTION: Compositions Isolated from Forage
TITLE OF INVENTION: Compositions Isolated from Forage
TITLE OF INVENTION: Compositions Isolated from Forage
TITLE APPLICANT: 1000.1074UC.1
GURRENT APPLICATION NUMBER: US/11/110,082
CURRENT FILING DATE: 2005-04-19
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        ----LGAVDHPLLGAAVPL 6205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7%; Score 86; 22.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 22.3%
Matches 92; Conservative
     TGTGDASGLG--
                                                                                                           US-10-793-626-2906
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APPLICANT: He, MIN
APPLICANT: Halti, Bradley A.
APPLICANT: Halti, Bradley A.
APPLICANT: Graziani, Edmund
APPLICANT: Graziani, Edmund
APPLICANT: Summers, Mia
APPLICANT: Rollowski, Kerry
APPLICANT: Rollowski, Kerry
APPLICANT: Rollowski, Kerry
APPLICANT: Rollowski, Kevin
TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
TITLE OF INVENTION: Polyketide
FILE REFERENCE: AM-10142605
FILE REFERENCE: AM-10142605
CURRENT APPLICATION NUMBER: US 60/664,483
FRIOR APPLICATION NUMBER: US 60/576,895
FRIOR FILING DATE: 2004-06-03
FRIOR FILING DATE: 2004-06-03
FRIOR FILING DATE: 2004-06-03
SOFTWARE: PATENTING DATE: 2004-06-03
SEQ ID NO 48
LENGTH: 7102
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                                                                                                                                                                                                                                                                                                                                                                    1029 RKWVIDSLKFRHEGTABLSGTVSMENSVPDVDIGAVFDKYRILSRP-----NRRLTVSGN 1083
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                                 -----TPSGKYIRIGYADKNEHPYVSIGRYMAD 296
                                                                                                                                                                                                                                                                                                                     RELAGSS----NDGPVGALGTPLMGEYA----GAVDRHYITLGAPLFVATAHPVTRKAL 385
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193 TIDNT--GGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPILGYA 250
                                                                                                                                                                                                               297 KGYLKLGQT-----SMCGIKSYMRQNPQRLAEVLGQNPSYIFF 334
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                                                                                                                                                  920 GSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRLNLTVADAE----
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1. Similarity 24.6%; Pred. No. 84;
67; Conservative 31; Mismatches
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                                                                                                      251 EDP-VELFFMHIQGSGRLK-
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Best Local S
Matches 67
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183 RIRQTGKNSGTIDNTGGT 200
                                                                                                                                            304 KVTLTSEBEARLKKSADT 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 IRIGYADKNEH----PYV-----SIGRYMAD----KGYLKLGQTSMQGIKSYMRQ-NPQ 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDMPNEFRLPNGLLLLEHTKVVQKSIYDHLHVTHEGQL-RIIFTPELKIMSWEFCSRRHD 381
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                                                                                                                                                                                                                                                                                                        22 OSKSIQTPPOPDISVINGPDRP-----VGIPDPAGTTVGGGGAVYTVVPHL----
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                                                                                                                                                                                                                                     ch 3.6%; Score 85; DB 7; Length 808;
l Similarity 21.1%; Pred. No. 10;
87; Conservative 54; Mismatches 166; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 RLAEVLGONPSYIFFRELAGSSNDGP-VGALGTPLMGEYAGAVDRHYITLGAP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/ldha_human
DATABASE ENTRY DATE: 1986-07-21
PRIOR APPLICATION NUMBER: 60/563,723
PRIOR FILING DATE: 2004-04-20
PRIOR PILING DATE: 2004-055,799
PRIOR FILING DATE: 2003-09-05
PRIOR PILING DATE: 2002-09-05
PRIOR PILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SEQ TWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 331
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APPLICANT: HOFfmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated proFILE REFERENCE: 21762
                                                                                                                                                                                    ORGANISM: Pestuca arundinacea
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US-10-878-556A-45
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Best Local S:
Matches 87
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APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: antibody fragments and fusions mediated plant disease FILE OF INVENTION: antibody fragments and fusions mediated plant disease FILE REFERENCE: 3581.01US01
CURRENT PAPLICATION NUMBER: US/10/512,184
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 66
LENGTH: 569
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Publication No. US20050244901A1
GENERAL INFORMATION:
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18.8%; Pred. No. 9.5;
tive 48; Mismatches 157; Indels 189; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: fusion protein protein in OTHER INFORMATION: comprising the leader peptide - chitinase - linker COTHER INFORMATION: - scFv VD2 - cmyc/His6.
                                                                                                                                                                                                                      Sequence 48, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 18.8°
Matches 91, Conservative
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460 TQTPL
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US-10-131-826A-112 ; Sequence 112, Application US/10131826A ; Publication No. US20050245730A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 PAGLRSGKALVRIROTGKNSGTIDNTGGTHTADLSRPPITARTTAIKGRFEGSRFLPYHT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PACQKI-MTCADPGBIAN--GHRTASDAGFPV-----GSHVQYRCLP--- 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
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PRIOR FILLING DATE: 1997-06-18

PRIOR PULICATION NUMBER: 60/059113

PRIOR PLILING DATE: 1997-08-26

PRIOR PLILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR PLILING DATE: 1997-09-18

PRIOR PLILING DATE: 1997-09-19

PRIOR PLILING DATE: 1997-09-19
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Best Local Similarity 20.9%; Pred. No. 18;
Matches 84; Conservative 38; Mismatches 109; Indels 170; Gaps
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                                                                                         Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                Watanabe, Colin K
                                                                                                                                                         Godowski, Paul J.
Gurney, Austin L.
Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                   Smith, Victoria
                                                                                                                           Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                     Wood, William
                                                                                                                                                                                                                                                                                                                     Tumas, Danie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapien US-10-131-826A-112
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---GPVGALGTPLMGEYAGAVDRHYITLGAPLFV 374
                                                                                                278 TSAANIGPALEDAQVGTVFHPKD----NRLSAWKFWALYAADTAGKIRLDDGAVEAVTSG 333
                                                                                                                                                                                                                                                                                                                                                        409 G------YGD-----RAGELAGK------QKTTGYVWQLLPNGMK 436
                                                                                                                                                                                                                                                                                                                                                                                                        56 GGG----AVYTVVPHLSLPHWAAQDFAKSLQ----SFRLGCANLKORQGWQDVCAQAFQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AAALALSLAAACSSDS----SSDSSSSSSSSGSEGGDNYVLVNGTEPQNPL---VPGNTNEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEACTBRIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - See File Wrapper or PALM.
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CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR PLING DATE: 1999-06-27
PRIOR PLING DATE: 1999-06-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1999-09-07
PRIOR PLING DATE: 1999-00-01
PRIOR PLING DATE: 1999-07-01
PRIOR PLING DATE: 1999-07-01
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-09
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Publication No. US20050244935A1
GENERAL INFORMATION:
                                                    -----NPSYIFFRELAGSSND--
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; ORGANISM: Cor
US-11-082-389-348
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            -- KWSDRVPKCALKYBPCLNPGVPENGYQ 782
                                                                                        --NPORLAE 323
                                                                                                                                137 VTGYYEPVLKGDDRRTAQARFPIYGIPD--DFISVPLPAGLR-----SGKALVRIRQTGK 189
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APPLICANT: Properly Burkhash
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schoe's Burkhash
APPLICANT: Schoe's Grader, Oskar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BG1-121CPCM
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT APPLICATION NUMBER: 00/606,740
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-03
PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-07-06
PRIOR PILING DATE: 1999-07-07-07-07-07-07-07-07-07-0
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Best Local Similarity 22.8%; Pred. No. 8;
Matches 97; Conservative 39; Mismatches 136; Indels 153; Gaps
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                                                                                                                                                                                                                                    324 ------VLGONPSYIPFRELAGSSNDGPVGA 348
                                                                                                                                                                                                                                                                                    842 GGNLALAILLPLGLVIVLGSG-VYIYYTKLQGKSLFGFSGS 881
                                                                            281 DKNEHPYVSIG---RYMADKGYLKLGQTSMQGIKSYMRQ
----GYSLEGAAMLTCYSRDTGTP---

    TYPE: PRT
    ORGANISM: Corynebacterium glutamicum
US-11-055-822-290

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Publication No. US20050260707A1
GENERAL INFORMATION:
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107 TPVHSPQAKQPPERYFTPWQV-AGNGSLAGTVTGYYEPVLKGDDR 150	
Qy 353 LWGEYAGAVDRHYITLGAPLFVATAHPVTRKALMRLIMA 391 Db 374 WSGEFSISYNADGGHOAWUDATANSIRNTLGIDAIGNPYPDPKSLRDDYTNRTIN 428 Qy 392 QDTGSAIDGANRVDYFWG-YGDEAGELAG 419 Db 429GAFRTGWQADYPSLGANFGFEAGENDG 459 RESULT 16	RESULT 17 US-11-096-051-4 US-11-096-051-4 Sequence 4, Application US/11096051 Publication No. US20050244868A1 Publication No. US20050244868A1 APPLICANT: Kekuda, Rameh APPLICANT: Kastelli, Luca APPLICANT: Rastelli, Luca APPLICANT: Tetemberg, Seth TILLE OF INVENTION: Ten-M3 Polypeptides and Polymucleotides and their Methods of Use TILLE OF INVENTION: Ten-M3 Polypeptides and Polymucleotides and their Methods of Use TILLE OF INVENTION: Ten-M3 Polypeptides and Polymucleotides and their Methods of Use TILLE OF INVENTION NUMBER: 10/038,854 PRIOR PLILING DATE: 2001-12-31 PRIOR PLILING DATE: 2001-06-04 PRIOR APPLICATION NUMBER: 10/455,772 PRIOR PLILING DATE: 2004-03-30 NUMBER OF SEQ ID NOS: 38 SEQ ID NO 4 IENTYRE: PRIT TYPE: PRIT TYPE: PRIT ORGANISM: Homo sapiens US-11-096-051-4
NUMBER OF SEQ ID NOS: 38 SOFTWARE: CuraseqList version 0.1 SEQ ID NO 14 LENGTH: 607 TYPE: PRT ORGANISM: Homo sapiens US-11-096-051-14	Query Match 3.5%; Score 81; DB 7; Length 2376; Best Local Similarity 19.4%; Pred. No. 1e+02; Matches 92; Conservative 50; Mismatches 137; Indels 196; Gaps 27; Qy 81 LQSFRLGCANLKNRQGWQDVCAQARQTPVHSRQAKQFFERYFTPWQV 127 Db 472 LQSSCQNQPYCRGLPDPQDIISQSLQSPSQQ-AAKSFYDRISFLIGSDSTHVIPGES 527
Query Match 3.5%; Score 81; DB 7; Length 607; Best Local Similarity 19.4%; Pred. No. 15; Matches 92; Conservative 50; Mismatches 137; Indels 196; Gaps 27; Qy 81 LQSFRLGCANLKORGWQDVCAQAFQTFVHSFQAKQFFERYFTPWQV 127	128 AGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRGT 187 1 1 1 1 1 1 1 1 1

Db	Query Match 3.5%; Score 81; DB 7; Length 2715; Best Local Similarity
	Query Match

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## APPLICANT: Ractachlan, Timothy K
## APPLICANT: Ractelli, Luca
## APPLICANT: Ractelli, Luca
## APPLICANT: Ractelli, Luca
## APPLICANT: Retenderg, Seth
## APPLICANT: Ettenderg, Seth
## TITLE OF INVENTION: Ten.M3 Polypeptides and Polymucleotides and their Methods of Use
## TITLE OF INVENTION: Ten.M3 Polypeptides and Polymucleotides and their Methods of Use
## TITLE OF INVENTION: Ten.M3 Polypeptides and Polymucleotides and their Methods of Use
## TITLE OF INVENTION: UNMBER: US/11/096,051
## CURRENT PILING DATE: 2003-06-04
## PRIOR APPLICATION NUMBER: 10/455,772
## PRIOR APPLICATION NUMBER: 60/557,978
## PRIOR APPLICATION NUMBER: 60/557,978
## PRIOR PILING DATE: 2004-03-30
## NUMBER OF SEQ ID NOS: 38
## SEQ ID NOS: 38
## SEQ ID NO 8
## SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --QDGMFDLVANGG------ASLTLV---FERSPFLTQYHTVWIPWNVFYVMDT 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%; Score 81; DB 7; Length 2725;
ilarity 19.4%; Pred. No. 1.2e+02;
Conservative 50; Mismatches 137; Indels 196;
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Publication No. US20050260581A1
GENERAL INFORMATION:
Application US/11096051
No. US20050244868A1
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APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Rlisabetta
                                                                      APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-096-051-8
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Best Local Similarity
Matches 92; Conserva
Sequence 8, Applicat
Publication No. US20
GENERAL INFORMATION:
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APPLICANT: MacLachlan, Timothy K
APPLICANT: Rastelli, Luca
APPLICANT: Pernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Stenberg, Seth
TITLE OF INVENTION: Ten.M3 Polypeptides and Polynucleotides and their Methods of Use
FILE REFERENCE: Attorney Docket No. Cura 967
CURRENT APPLICATION NUMBER: US/11/096,051
CURRENT FILING DATE: 2001-12-31
FRIOR APPLICATION NUMBER: 10/455,772
FRIOR FILING DATE: 2003-06-04
FRIOR FILING DATE: 2004-03-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE: CuraSequist version 0.1
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                         -----NRLIMAQDTGSAIDGAVRVDYFWGYGDEAGBLAGKQKTTGYVWQLLPNG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 LOSFRIGCANLKNROGW---ODVCAOAFOTPVHSFOAKOFFER--
                                                       |:|: | |
1179 NGQADGNKLLAPVALACGIDGSLYVGDF--
                                                                                                                                                                                    Sequence 10, Application US/11096051
Publication No. US20050244868A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                   US-11-096-051-10
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US-11-096-051-8
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Matches 92
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  299 DNAGTVKGNG-----EH----HWKTTGTNSHIGSTAVRLANNEGDANNGONVTFEDNG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 TLVLDQNINQGAGGLPPKGDYTVKGANNDITWLGAGIDVADGKKVVWQVKNPNGDRLAKI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 GKGTLEINGTGVNOGQLKVGDGTVILNQKADSNQKVQA-PSQVGIVSGRGTLVLNSPDQI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 ISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSRPPITARTTAIKGRFEGSRF 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 IRIGYADKWEHPYV----SIGRYMADKG-----YLKLGQTSMQGIKSYM-RQNPQRLA 322
                                                                                                                                                                                                                                                                                                3.4%; Score 79.5; DB 6; Length 1565; 21.2%; Pred. No. 77; ive 40; Mismatches 140; Indels 143;
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: PONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPRENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PPLICATION NUMBER: GB-0103424.8
PRIOR PLILING DATE: 2001-02-12
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                 CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 2704
LENGTH: 1565
                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2704
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SOFFWARS SeqWin99, version 1.04
SEQ ID NO 1784
LENGTH: 392
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US-10-467-657-1784
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87; Conservative
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US-10-467-657-1784
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Best Local S
Matches 87
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Score 78; DB 6; Length 392; Pred. No. 15;

3.3%;

Query Match Best Local Similarity

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221 FEGSRFLP----YHTRNQINGGA-----LDGKAPILGYAEDPVELFFMH--IQGSGRLKT 269
                                                                                                                                                                                                                                                   126 NNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVG-MHI 184
                                                                                                                                                                                                                                                                                                                    270 PSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQNP 329
                                                                                                                                                                                                                                                                                                                                                                                 185 ANGMYGLILVEPKEGLPKVDKEFYIVQGDFYTKGKKGAQGLQ-----PFDMDKAVAEQP 238
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P9330RIC128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
                                                         169 VPLPAGLRSGKALVRIR----QTGKNSGTIDNTGGTHTADLSRPPITAR---TTAIKGR
36; Gaps
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 144
LENGTH: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 SYIFFRELAGSSNDGPVGAL-GTPLMGEYAGAVDRHYITLGAPLFVATAHPV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
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PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beresini, Maureen
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney, Austin L.
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a Complex

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US-10-793-626-2774

Sequence 2774, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

TITIES OF INVERTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PUJ480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT PILING DATE: 1999-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

NUMBER OF SEQ ID NOS: 4472

SOFTWARE PATENTING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SEQ ID NO 2774
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| | | | | : | : | 3431
| 3431 RRRFWAASLRQTPGTAEFDHPLLGAVLPLPDSGGGLLTGVLTLAGQPWL-AEHSVAGVVL 3431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AKQFFERYF------TPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQAR 156
                                                                                                                                                                                                                                   APPLICANT: He, Min
APPLICANT: Hucul, John
APPLICANT: Hucul, John
APPLICANT: Hacul, John
APPLICANT: Hacul, John
APPLICANT: Hacily Melisa M.
APPLICANT: Summers, Mis
APPLICANT: Summers, Mis
APPLICANT: Summers, Mis
APPLICANT: Summers, Mis
APPLICANT: Summers, Mis
APPLICANT: Milowski, Kerry
APPLICANT: Nolowski, Kerry
APPLICANT: Pong, Kevin
TITLE OF INVENTION: Polyketide
FILE REFERENCE: AM-10426US
CURRENT APPLICATION NUMBER: US/11/143,980
CURRENT PLING DATE: 2005-06-03
PRIOR PILING DATE: 2005-06-03
PRIOR PILING DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Petentin version 3.3
LENGTH: ST12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 VGGGGAVYTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 PPIYGIPDDFISVPLPAGLRSGKALV 182
                                  Sequence 47, Application US/11143980 Publication No. US20050272133A1 GENERAL INFORMATION:
       418 AGKOKTTGYVWQLLPNGMKP 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces sp.
                                                                                                                                                   US-11-143-980-47
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                                                                                            243 KAPILGYAEDPVELF--FMHIQGSGRLKTPSGKYI---RIGYADKWEHPYVSIGRYMAD- 296
                                                                                                                                           52 KAPTSTRFSDAIRAFQWVSQLPVSGVLDRATLRQMTRPRCGVTDTNS--YAAWAERISDL 109
                                                                                                                                                                                           297 ------KGYLKGGOTSMQGIKSYMRQN-PQRLAR-------VLGQNPSYIF 333
                                                                                                                                                                                                                                110 FARHRTKMRRKKRFAKQGNKWYKQHLSYRLVNWPEHLDFBAVRGAVRAAFQLWSNVSALE 169
                                                                                                                                                                                                                                                                                       334 FREL-------AGSSNDGPVGALG---TPLMGEYAGAVDRHYI---T 367
                                                                                                                                                                                                                                                                                                                                    170 FWEAPATGPADIRLTFFQGDHNDGLGNAFDGPGGALAHAFLPRRGEAHFDQDERWSLSRR 229
                                                                                                                                                                                                                                                                                                                                                                                    368 LGAPLFVATAHPV-----TRKALNRLIMA------QDTGSAIDGAVRVDYFWGY---G 411
                                                                                                                                                                                                                                                                                                                                                                                                                    230 RGRNLFVVLAHBIGHTLGLIHSPAPRALMAPYYKRLGRDALLSWDDVLAVQSLYGKPLGG 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 KETFYLSSNGVQTDLVAGRLK---GETAKVDILDKEGNVLVAKGKRITAKNIRDITNAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 GSRFLPYHTRNQINGGALD-----GKAPI-----LGYAEDPV----
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                                                    74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 78; DB 6; Length 1394; Best Local Similarity 19.7%; Pred. No. 89; Matches 63; Conservative 40; Mismatches 97; Indels 1:
    DB 6; Length 520;
Query Match 3.3%; Score 78; DB 6; Length 520 Best Local Similarity 23.9%; Pred. No. 23; Matches 64; Conservative 23; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7930, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNATI Vega
APPLICANT: MASIGNATI Vega
APPLICANT: MASIGNATI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 DEAGELAGKOKTTGYVW-QLLPNGMKPE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 SVAVQLPGKLFTDFETWDSYSPQGRRPE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
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ORGANISM: Neisseria gonorrhoeae
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US-10-467-657-7930
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|| || || GGVAVDQAHEAMDELTERPH-PYPRWLA---TAGAAGPALGVAMLLG--GTWLTCVLAAV 188
                                                                                                                                                                                      188 GKNSGTIDNTGGTHTADLSRPPITARTT-AIKGRPEGSRPLPYHTRNQINGGALDGKA-P 245
                                                                                                                                                                                                                                                                            332 İASYAP-----LRSVATAGLSAĞLAB-----LVLİĞLGAAĞFĞRVVATWT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 GGVAVDQAHEAMDELTERPH-PYPRWLA---TAGAAGFALGVAMLLG--GTWLTCVLAAV 188
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189 TSGVIDRLGRLLINRIGTPLFFQRVFGAGIATLVAVAAYLIAGQDPTALVATGIVVLLSGM 248
                                                                                                                                                          131 ---GSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 AAIĞVGFLATLISIRRÖAPALVTATAĞIMPMLPGLAVFRAVFAFAVNÖTPDGGLTQLLEA 431
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                                                                                                 56 GGGAV-----YTVVPHLSLPHWAAQDFAKGLQSFRLGCANLKNRQGWQDVCAQAFQ
                                                                                                                                                                                                                                                                                                                                         246 ILGYAEDPVELPFMHIQGSGRIKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQT
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APPLICANT: Driggers, Edward M.
APPLICANT: Madden, Kevin T.
APPLICANT: O'Toole, George
APPLICANT: O'Toole, George
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Joshua
APPLICANT: Worgey, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
CURRENT APPLICATION NUMBER: US/10/4-06-01
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 364
SOFTWARE FRACESEQ for Windows Version 4.0
SEQ ID NO 105-
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMOGIK-----SYMRONPORLAEVLGONPSY----IFFRELAGSSNDGPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 529;
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                                                                  107 TP------VHSPQAKQFFERYF------TPWQVAGN--
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                                                                                                                                                                                                     249 TLVGŚMQDAVTGYMLTAĽ----AŘLGDÁLF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10858730 . US20050255568A1
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Doten, Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bailey, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 105, Applic; Publication No. US20; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-858-730-105
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Matches
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                                                                                                                                                                                                                                                                                          117 ILRAVIEGETVRLVKKFOTDDMLTQIKTYPITHMSLV--PQTLKWLMD-AGLT----- 166
                                                                                                                                                                                                                                                                                                                                       YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVH-SFQAKOFFE 119
                                                                                                                                                                                                                                                                                                                                                                    167 ------QPF--SLEKILLGGAKLSPQLIEQ---ALTYRLPVYNSFGMTETCS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 QFLTA-----SPQMLKERFDTVGKPSENVEVKIKNPNAYGH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKALVRIRQTGKN-----SGTIDNTGGTHTADLSRFPITARTTAIKGRFE---- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GKAPILGYAEDP-----VELF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 GGENIYPY----QIETIAKDFEGIEDAVCVGISDDTWGQVPILYYVTNQDINQTELIEHF 355
                                                                                                                                                                                                                                               5 LFRAALYGIAAAILAACQS----KSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                 RYFTPWQVAGNGSLAGTVTGYYBPVLKGDDRRTAQARPPIYGIPDDFISVPL--PAGLRS
                                                                                                                                                                                                       Gaps
                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
                                                                                                                                                       Query Match
3.3%; Score 77.5; DB 6; Length 400;
Best Local Similarity 20.6%; Pred. No. 17;
Matches 70; Conservative 37; Mismatches 116; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Trucheart, Joshua
APPLICANT: Trucheart, Joshua
APPLICANT: Walbridge, Michael J.
APPLICANT: Vorgey, Peter S.
APPLICANT: Vorgey, Peter S.
TITLE OF INVENTION: PRODUCTION
FILE REPRENCE: 14184-030001
CURRENT APPLICATION NUMBER: 105/10/858,730
CURRENT PILING DATE: 2004-06-01
PRIOR PILING DATE: 2003-05-30
PRIOR PILING DATE: 2003-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 FMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENHL---ARYKIPK-KYYQV-----KSLPYTSTGKLQRKK 386
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22.2%; Pred. No. 26;
iive 35; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 -GSRFLPYHTRNQINGGALD-----
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US-10-858-730-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 104, Application US/10858730 Publication No. US20050255568A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doten, Reed
Driggers, Edward M.
Madden, Kevin T.
                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
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O'Toole, George
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Best Local Similarity
Matches 92; Conserva
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Job time

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2161 ------PSVATVGSICDIN-LKIPEINSSDMSAHVTSPSGRVTEABIVPMGKNSHCVR 2211
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US-10-821-224-1262

US-10-821-224-1262

US-10-821-224-1262

Sequence 1262, Application US/10821234

PUblication No. US20060255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
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APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANTON NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SEQ ID NOS: 1704

SEQ ID NO 1262

SEQ ID NO 1262

SEQ ID NO 1262
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                                                           188 GKNSGTIDNTGGTHTADLSRPPITARTT-AIKGRPEGSRFLPYHTRNQINGGALDGKA-P 245
                                                                                            289 ------GVINAGIQIELHVDATTTLATPG-------MPLPILVAVSGAALSGVCLT 331
                                                                                                                                                                      306 SMQGIK-----SYMRQNPQRLAEVLGQNPSY----IFFRELAGSSNDGPVG----- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DDRRTAQARFPIYGIPDDFI--- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 -----SVPLPAGLRSGKALVRI------ROTGKNSGTIDNTGGTHTADLS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 RFPIT----ARTTALKGR----FEGSRFLPYHTRNQINGG---ALDGKAPI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 LGYAED--------PVELPFMHIQGSGRLKTPSGKYIRI 277
                                                                                                                                                                                                                                                                 372 AAIGVGFLATLISIRRQAPALVTATAGIMPMLPGLAVFRAVFARAVNDTPDGGLTQLLEA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 GYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEV----LGQNPSYIF 333
                                                                                                                                           246 ILGYAEDPVELFFWHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
3.3%; Score 77.5; DB 6; Length 2657;
Best Local Similarity 20.1%; Pred. No. 2.4e+02;
Matches 71; Conservative 39; Mismatches 101; Indels 143; Gaps
                                                                                                                                                                                                                                                                                                       348 ----ALGT-PLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGS 396
                                                                                                                                                                                                                                                                                                                                   334 F-------RELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAP 371
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; ORGANISM: Homo sapiens
US-10-821-234-1262
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Search completed: December 30, 2005, 08:28:54

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Sequence 776, App
Sequence 1810, Ap
Sequence 65, Appl
Sequence 47, Appl
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66, Appl
112, App
348, App
348, App
14, Appl
4, Appli
2, Appli
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8108, Ap
334, App
48, Appl
2906, Ap
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                                                                    (without alignments)
412.820 Million cell updates/sec
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                                                                                                                    1 MKKYLFRAALYGIAAAILAA......KTTGYVWQLLPNGMKPEYRP 441
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                                                         08:25:13 ; Search time 8 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-512-184-65
US-10-467-657-8108
US-10-467-657-334
US-11-13-980-48
US-11-10-082-38
US-10-73-658-45
US-10-512-184-66
US-10-13-184-66
US-10-13-184-66
US-10-13-184-66
US-10-13-184-66
US-11-096-051-14
US-11-096-051-14
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US-10-467-657-1784
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                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-096-051-10
US-11-096-051-8
                                                                                                                                                                     57103 seqs, 7488799 residues
                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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                                                         December 30, 2005,
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seq length: 200000000
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2340
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Match ]
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Maximum DB
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Sequence 47, Appl	Sequence 2774, Ap	Sequence 104, App	Sequence 105, App	Sequence 1262, Ap	Sequence 5866, Ap	Sequence 68, Appl	Sequence 37, Appl	Sequence 1632, Ap	Sequence 8400, Ap	Sequence 127, App	Sequence 52, Appl	Sequence 53, Appl	Seguence 54, Appl	Sequence 55, Appl	Sequence 29, Appl	Sequence 2310, Ap	Sequence 258, App	Sequence 5134, Ap	Sequence 1592, Ap	
US-11-143-980-47	US-10-793-626-2774	US-10-858-730-104	US-10-858-730-105	US-10-821-234-1262	US-10-467-657-5866	US-10-131-826A-68	US-11-135-855-37	US-10-793-626-1632	US-10-467-657-8400	US-10-485-517-127	US-11-115-639-52	US-11-115-639-53	US-11-115-639-54	US-11-115-639-55	US-11-170-653-29	US-10-467-657-2310	US-11-055-822-258	US-10-467-657-5134	US-10-821-234-1592	
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5712	400	529	529	2657	287	745	745	372	1006	1263	1394	1394	1394	1394	219	405	423	457	782	
3.3	3.3	3.3	3,3	3.3	3.3	3.3	3.3	3.2	3.2	3.2	3.2	3.5	3.2	3.2	3.2	3.2	3.2	3.2	3.2	
78	77.5	77.5	77.5	77.5	76.5	76.5	76.5	16	16	16	92	16	16	16	75.5	75.5	75.5	75.5	75.5	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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61 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 YFTPWQVAGNGSLAGTVTGYYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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             Sequence 776, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Neisseria gonorrhoeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
US-10-467-657-776
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Ne1
US-10-467-657-776
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Matches 422;
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 776
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                                                                                        195 YVAIGQKDSTVRANVEKLR------QAGALDYTIVVSASAADPAPLLYIAPYSGVT 244
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                                                                    VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGK 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 MGEEFMFNGKHVLIVYDD--------LTKQAAAYRELSLLLRRPPGREA- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 VLGQNPSYIFF-----RELAGSSND----GPVGALGTPLMGEYAGAVDRH------ 364
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                                                                                                                                                                                                                                                                                                           APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480U2
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1810
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 94; DB 6; Length 503; 20.2%; Pred. No. 0.85;
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                                                                                                                                                                                                                                                          ; Sequence 1810, Application US/10793626; Publication No. US20050255478A1; GENERAL INFORMATION:
                                                                                                                                                                   OKTIGYVWOLLPNGMKPEYRP 468
                                                                                                                                         OKTTGYVWQLLPNGMKPEYRP 441
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ORGANISM: Artificial Seguence
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Matches 76; Conserv
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US-10-793-626-1810
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; Sequence 65, Application US/10512184; Publication No. US20050244901A1

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APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: antibody fragments and fusions mediated plant disease FILE OF INVENTION: resistance against fungi FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
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CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.0%; Score 94; DB 6; Length 576;
Best Local Similarity 19.8%; Pred. No. 1;
Matches 102; Conservative 50; Mismatches 156; Indels 206; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising chitinase - linker OTHER INFORMATION: scFv CWPD2.
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LENGTH: 576
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RESULT 6
US-10-467-657-334
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LENGTH: 1389
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                                                                                                                                                                                                                                                                                                                                                                                                                   316 DCYNORPPAVDGGGGGGGGG---GSAAQPAMAAVTLDESGGGLQTPGG-------
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                               21 CQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAVYT------VVPHLSLPHWAA
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                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: comprising the leader peptide - chitinase - linker OTHER INFORMATION: - scFv CWPD2 - cmyc/His6.
                                                                                                                                                                                                                                                                                                                              ODF-----GW-----GW----
                                                                                                                                                                                            Query Match 4.0%; Score 94; DB 6; Length 625;
Best Local Similarity 19.8%; Pred. No. 1.2;
Matches 102; Conservative 50; Mismatches 156; Indels 206;
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APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GLSLVCKG---SGFDFSSDTMMWVRQAPGKGLEF----
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
ERQ ID NO 8108
LENGTH: 473
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; Publication No. US20050260581A1
                                                                TYPE: PRT
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
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US-10-467-657-8108
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                                                                                                                                                         US-10-512-184-47
                              SEQ ID NO 47
LENGTH: 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ICY-YCGCNKIITKDKSRADTYIEYLEKEMELLAPHLNGRHQ-LAQLHFGGGTPTFLSDE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 ---VATAHPVTRKALNRLIMAQDTGSAIDGA-----VRVDYFWGYGDEAGELAGKQKT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 -----LPHWAAQDFAKSLQSFRLGCA---NLKNRQ----GWQDVCAQA--FQTPVHSFQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        705 GGINRELTRWKG-----SIGILDIĞGAFNLKLQNRMTLEAGAEHVAASAANWQAMGGSLN 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 1919 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 NEHPYVSIGRYMA-DKG----YLKLGQTSMQGIKSYMRQNPQRLAEVL--GQNPSYI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FFR-----ELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLF----
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                          82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 AKOFFERYFTPWO----VAGNGSLAG----TVTGYYEP-----VLKGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1389;
                                                                                                                                                                Length 473;
                                                                                                                                                                                                                                                                          90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MAISGRANI Vega
APPLICANT: MAISGRANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GIPDPAGTTVGGGGAVYTVVPHLS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%; Score 90.5; DB 6; 1
20.4%; Pred. No. 7.1;
Live 51; Mismatches 179;
                                                                                                                                                           DB 6;
1.2;
                                                                                                                                                                3.9%; Score 92; DB (20.7%; Pred. No. 1.2; ive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : ||: | |: |
241 TIDTVLSLDPDRLALYHYAHLPHVFKPQRR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 T------GYVWQLLPNGMKPEYR 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 334, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
ORGANISM: Neisseria gonorrhoeae US-10-467-657-8108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Neisseria gonorrhoeae
US-10-467-657-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: SegWin99, version 1.04
                                                                                                                                                                Query Match 3.9% Best Local Similarity 20.7% Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 20.4*
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 9218
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Sequence 2906, Application US/10793626
; Sequence 2906, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; TITLE OF INVERTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVERTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR APPLICATION NUMBER: 60/164,258
; RIOR RILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE PATENTIN Ver. 2.1
; SEQ ID NO 2906
; LENGTH: 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 VNKVKDIGGKARDIGGTTPDKAKDIGTKALDKAKDVSSTVIKGIGDVFDYV----GHPM 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 ARLLTGOFTLFFMHLSKILKQGKIKAGEPWAKTGNSGOWTTGPHVHFQVERGRHDDITNR 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1310 GTVNPAKWLKGH---GGGKVGGSGSVNARRAIQRAQSILGGRYKSSYITEQMMRVAKRES 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1029 PKGSSVYSGAQT----HAILSNSGYDTKKKKLPKFSKG---TKKKDGILDVISSGVKND 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHSF-----QAKQFFERYFTPWQVAGNGSL------AGTVTGYYEPVLKGDDR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 SRFPIT-----ARTTAIKGRFEGSRF----LPYHTR-NQINGGALD----GKAPI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 PAGTTVGGGGGAVYTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 RTAQARFPIYGIPDDFI-SVPLPAGLRSGKALVRIRQTG----KNSGTIDNTGGTHTADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 LGYAEDPVELFFMHI-----QGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.7%; Score 86; DB 6; Length 1572;
22.3%; Pred. No. 21;
.ive 44; Mismatches 171; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AGSSNDGPVGA-LGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KGYLKLGQTSMQGIKSY-MRQNPQRLAEVLG--QNPSYIFFREL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/11110082;
Publication No. US20050266558A1
GENERAL INFORMATION:
APPLICANT: Demmer, Jercen
APPLICANT: Hall, Claire
APPLICANT: Norriss, Michael Geoffrey
APPLICANT: Norriss, Michael Geoffrey
TITLE OF INVENTION: Compositions Isolated from Forage
TITLE OF INVENTION: Grasses and methods for their use.;
FILE REPERENCE: 11000.1074Ucl
CURRENT APPLICATION NUMBER: US/11/110,082
     6181 TGTGDASGLG-----LGAVDHPLLGAAVPL 6205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.3*
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-110-082-38
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APPLICANT: Halti, Bradley A.

APPLICANT: Halti, Bradley A.

APPLICANT: Halti, Bradley A.

APPLICANT: Summers, Main

APPLICANT: Summers, Mia

APPLICANT: Summers, Mia

APPLICANT: Nulowski, Kerry

APPLICANT: Pong, Kevin

TITLE OF INVENTION: Polyketide

TITLE OF INVENTION: Polyketide

TITLE OF INVENTION: Polyketide

TITLE OF INVENTION: Polyketide

CURRENT PILING DATE: 2005-06-06-06

CURRENT PILING DATE: 2005-06-03-23

PRIOR FILING DATE: 2005-03-23

PRIOR PILING DATE: 2004-06-03

NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6080 FÖSTVEALIGOGHTVFVEASPHPVLTVGVQDT-------ADAMETPIVATGS 6124
                                                                                                                                                                                                                                                              969 RNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSINGDKLYYRNQTQGIILDNGSLRSHIAG 1028
                                                                                                                                                                                                                                                                                                                                                                    1029 RKWVIDSLKFRHEGTAELSGTVSMENSVPDVDIGAVFDKYRILSRP-----NRRLTVSGN 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 -QINGGALDGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 YMADKGYLK----LGQTSMQGIKSYMRQNPQRLAEVLGQN----PSYIFFRE---LAGS 340
                                                                                                         ------TPSGKYIRIGYADKNEHPYVSIGRYMAD 296
                                                                                                                                                                                                             SMQGIKSYMRQNPQRLAEVLGQNPSYIFF 334
                                                                                                                                                                                                                                                                                                                 335 RELAGSS----NDGPVGALGTPLMGEYA----GAVDRHYITLGAPLFVATAHPVTRKAL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AGNGSLAGTVTGYYEPVLKGDDRRTAQARFP-IYGIPDDFISVPLPA-GLRSG--KALVR 183
193 TIDNT--GGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPILGYA 250
                                                   874 NMANTPLGGRITASLPDL-----GALK-----PFLPAAAQNIT--GSLNASAQIGGRV 919
                                                                                                                                                    920 GSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRLNLTVADAE------AF 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 IRQTGKNSGTIDNTGGTHTADLSRF-PITAR----TTAIKGRFEGSRFLPYHTRN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GLFGSQKSS 1113
                                                                                                                                                                                                                                                                                                                                                                                                                        386 NRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 SNDGPVGALGTPLMGEYAGAVDRHYITLGAPL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 89.5;
24.6%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 48, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : | :: |
1084 TRLRYSPQKGISVTGMIKTDQ--
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                                                                                                    251 EDP-VELFFMHIQGSGRLK---
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APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 1581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
         127 VAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPI---YGIPDD-FISVPLPAGLRSGKALV 182
                                                                                                    ------QDVCAQAFQTPVHSFQAKQFFERYFTPWQVAGN-----GSLAGT----- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 FNQERGAASDYCSPNSQWP--CAPGKKYFGR--GPIQISYNYNYGPAGRAIGTDLLNNPD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VTGYYEPVLKGDDRRTAQARFPIYGIPDDF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 ISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCYNORPFAVDGGGGSGGG---GSAAQPAMAQIQLVQSGPELKKP-GETVKISCKVSGDN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --YADKNEHPYVSIGRYMADKGYLKLGQTSM 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYIT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDTATYF-----CARFLG-NPYYVM--DYWGQGTSVTVSAGGGGGGGGGGDSDVLM 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 COSO------CNGCSGGGTPVPVPTPTG---GGVSSIISQSLFDQMLLHRNDAACQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 CQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAVYT------VVPHLSLPHWAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 LPYHTRN-QINGGALDGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising chitinase - linker OTHER INFORMATION: scFv VD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 3.6%; Score 83.5; DB 6; Length 569; Similarity 18.8%; Pred. No. 8.4; 91; Conservative 48; Mismatches 157; Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 66, Application US/10512184; Publication No. US20050244901A1; GENERAL INFORMATION:
                                                                                                                                                                183 RIRQTGKNSGTIDNTGGT 200
                                                                                                                                                                                              304 KVTLTSEEEARLKKSADT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 66
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 SQ-----DTWRCDICNTHAGKGHEA-----TYEIL-----PRLCQIRFD-QGVIDEYLF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 LDMPNEFRLPNGLLLLEHTKVVQKSIYDHLHVTHEGQL-RIIFTPELKIMSWEFCSRRHD 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYHTRN----QIN-----GGALDGKAPILGYAEDPVELFFWHIQGSGRLKTPSGKY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 IRIGYADKNEH----PYV-----SIGRYMAD----KGYLKLGQTSMQGIKSYMRQ-NPQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 SLPHWAAQDFA-KSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFERYFTPWQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 VPLPAGLRSGKALVRIRQTGKNSGTI-DNTGGTHTADLSRFPITARTTAIKGRFEGSRFL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SLPHWAA---QDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQ----TPVHSFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSKSIQTFPQPDTSVINGPDRP-----VGIPDPAGTTVGGGGAVYTVVPHL----
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                                                                                                                                                                                                                                                                                                                                                                 54; Mismatches 166; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 17;
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                                                                                                                                                                                                                                                                                              3.6%; Score 85; DB 7; Length 808; Conservative 54; Mismathh.
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Publication No. US20550266399A1
GENERAL INFORMATION: US20550266399A1
TTLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.6%; Score os.., ..., -
Best Local Similarity 23.9%; Pred. No. 4;
Matches 33; Conservative 26; Mismatches 62;
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DATABASE ACCESSION NUMBER: sw hum/ldha_human
DATABASE ENTRY DATE: 1986-07-21
PRIOR APPLICATION NUMBER: 60/563,723
PRIOR FILING DATE: 2004-04-20
PRIOR PILING DATE: 2004-04-20
PRIOR APPLICATION NUMBER: 10/655,799
PRIOR PILING DATE: 2003-09-05
PRIOR PILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PastSEQ for Windows Version 4.0
SCACTOL IN 808
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Festuca arundinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Best Local Similarity
Matches 87; Conserv
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US-10-878-556A-45
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PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
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PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
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                                                                                                                                                                                                                 Gerritsen, Mary E.
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Wood, William
                                                                                                                                                                                                                                                                                    Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                         Sherwood, Steven
                                                                                                          Desnoyers, Luc
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
                                                                                                                                                                                Gao, Wei-Qiang
                                                                         DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumas, Danie
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US-10-131-826A-112
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Best Local Similarity
Matches 84; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                                     APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT PILING DATE: 204-10-22
NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QDVCAQAFQTPVHSFQAKQFFERYFTPWQVAGN-----GSLAGT----- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VIGYYEPVLKGDDRRTAQARFPIYGIPDDF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 ISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 IN----GGLECGR------GQDGRVADRIG------FYKRYCDLLGVSYGDNL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----YADKNEHPYVSIGRYMADKGYLKLGQTSM 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 QGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYIT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: comprising the leader peptide - chitinase - linker OTHER INFORMATION: - scFv VD2 - cmyc/His6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 83.5; DB 6; Length 618;
18.8%; Pred. No. 9.5;
tive 48; Mismatches 157; Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 QDF-----AKSLQSF-RLGCANLKNRQ-------GW-----
                                                                                                                                                                         ; Sequence 48, Application US/10512184; Publication No. US20050244901A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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91; Conservative
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460 TQTPL 464
                                                                                                                                           US-10-512-184-48
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LENGTH: 618
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Matches 9
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; Sequence 112, Application US/10131826A ; Publication No. US20050245730A1

RESULT 13 US-10-131-826A-112

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330HZ128
CURRENT APPLICATION NUMBER: US/10/131,826A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GIAAAILAACQSKSIQTFPQPDTSVI-NGPD-----RPVGIPDPAGTTVGGGGAVY---
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20.9%; Pred. No. 18;
rative 38; Mismatches 109; Indels 170; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 112
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---GPVGALGTPLMGEYAGAVDRHYITLGAPLFV 374
                                                                                                     220 LFDKNPTDPTAKFISEVR-DGNDLKGVIAGDGGKVGTGGMASKVSAA-RLASRSGVPVLL 277
                                                                                                                                                                   --HPVTRKALNRL-----IMAQDTGSAI---DGAVRVDYFW 408
                                                                                                                                                                                                                          278 TSAANIGPALEDAQVGTVFHPKD----NRLSAWKFWALYAADTAGKIRLDDGAVEAVTSG 333
                                                                                                                                                                                                                                                                                           ---- QKTTGYVWQLLPNGMK 436
                                                                                                                                                                                                                                                                                                                                                   334 GKSLLAVGITEIIGDFQQGEIVEILGPAGQIIGRGEVSYDSDTLQSMVGMQTQDLPDGMQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schroder, Hartward
APPLICANT: Schroder, Hartward
APPLICANT: Schroder, Hartward
APPLICANT: Schroder, Oskar
APPLICANT: Schroder, Hartward
APPLICANT: Schroder, Oskar
APPLICANT: Schroder, Oskar
TITLE OF INVENTION: CORYNDEACTENIUM GLUTAMICUM GENES ENCODING PROFIENS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-131CPCN
CURRENT FILING DATE: 2005-03-16
FRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
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PRIOR FILING DATE: 1999-08-31
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19.7%; Pred. No. 13;
tive 64; Mismatches 169; Indels 184;
                                                                                                                                                                                                                                                                                        409 G-----YGD------EAGELAGK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 348, Application US/11082389
Publication No. US20050244935A1
GENERAL INFORMATION:
                                             -----NPSYIFFRELAGSSND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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Best Local Similarity 19.7%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             437 PEYRP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 ---RP 395
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                                                                    ---NPQRLAE 323
                                                                                                     137 VTGYYEPVLKGDDRRTAQARFPIYGIPD--DFISVPLPAGLR-----SGKALVRIRQTGK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 NSGTIDNTGGTHTADLSRFPITARTTAIKGRFE-GSRFLPYHTRNQINGGALDGKAPILG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 ADKGYLKLGQTSMQGIKSYMRQNP-----QRLAEVLGQ------ 327
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22.8%; Pred. No. 8;
ive 39; Mismatches 136; Indels 153; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ALGGET, BUILTIAGG
APPLICANT: ALGGET, BUILTIAGG
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Aberhauer, Gregor
TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BG1-121CPCN
CURRENT APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
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PRIOR PILING DATE: 1999-07-08
PRIOR PILICATION NUMBER: DE 19931419.5
PRIOR PILING DATE: 1999-07-08
                                                                                                                                                                                         -----VLGQNPSYIFFRELAGSSNDGPVGA 348
                                                                                                                                                                                                                                 842 GGNLALAILLPLGLVIVLGSG-VYIYYTKLQGKSLFGFSGS 881
                                                             281 DKNEHPYVSIG---RYMADKGYLKLGQTSMQGIKSYMRQ--
----GYSLEGAAMLTCYSRDTGTP----
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PRIOR FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 290, Application US/11055822
Publication No. US20050260707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kroger, Burkhard
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Best Local Similarity
Matches 97; Conservi
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人物 等法教学徒 不久

232RNQINGGALDGKAPILGYAEDPVELFF	Qy 357 YRAALDENATAHPYT	## APPLICANT: Usersel, Luca ### APPLICANT: Vernet, Corine ### APPLICANT: Vernet, Corine ### APPLICANT: Ettenberg, Seth ### TITLE OF INVENTION: Ten-M3 Polypeptides and Polymucleotides and their Methods ### TITLE OF INVENTION: Ten-M3 Polypeptides and their Methods ### TITLE OF INVENTION: Ten-M3 Polypeptides and their Methods ### CURRENT APPLICATION NUMBER: US/11/096,051 ### CURRENT PILING DATE: 2001-03-30 ### PRIOR APPLICATION NUMBER: 10/455,772 ### PRIOR APPLICATION NUMBER: 10/455,772 ### PRIOR FILING DATE: 2003-06-04 ### PRIOR PILING DATE: 2004-03-30 ### PRIOR FILING DATE: 2004-03-30 ### TITLE TITLE TENT ### TITLE TENT ### TITLE TENT ### TITLE TENT ### TITLE TENT ### TITLE TENT ### TITLE TENT ### CORTANTAN Home sapiens ### US-11-096-051-4	Query Match 3.5%; Score 81; DB 7; Length 2376; Best Local Similarity 19.4%; Pred. No. 1e+02; 196; 37; Matches 92; Conservative 50; Mismatches 137; 196; Gaps 27; Qy 81 LQSFRLGCANLKNRQGWODVCAQAFQTFVHSFQAKQFFERYFTPWQV 127 1 1 1 1 1 1 1 1 1 1	128 AGNGSLAGTVTGYZEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRGT 187
107 TPVHSFQAKQFFERYFTPWQV-AGNGSLAGTVTGYYEPVLKGDDR	Qy 266 RLKTPGGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGTKS- 312 1	RESULT 16 US-11-096-051-14 is Sequence 14, Application US/11096051 is Publication No. US20050244868A1 is GENERAL INFORMATION: APPLICANT: Kekuda, Ramesh is APPLICANT: MacLachlan, Timothy K APPLICANT: Retelli, Luca APPLICANT: Retelli, Luca APPLICANT: Retelli, Luca APPLICANT: Retelli, Luca APPLICANT: Retelli, Luca APPLICANT: Retelli, Luca APPLICANT: Retelli, Luca APPLICANT: Vernet, Corine APPLICANT: Vernet, Corine APPLICANT: Vernet, Corine APPLICANT: Vernet, Corine APPLICANT: Vernet, Corine APPLICANT: Norman Polymorleotides and their Methods of Use FILE REFERENCE: Attorney Docket No. Cura 967 CURRENT FILING DATE: 2005-03-30 PRIOR FILING DATE: 2001-12-31 PRIOR FILING DATE: 2001-12-31 PRIOR FILING DATE: 2003-06-04 PRIOR APPLICATION NUMBER: 10/455,772 PRIOR APPLICATION NUMBER: 60/557,978	; PRIOR FILING DATE: 2004-03-30 ; NUMBER OF SEQ ID NOS: 38 ; SOFTWARE: CuraSequist version 0.1 ; SEQ ID NO 14 ; LENGTH: 607 ; TYPE: PRT ; ORGANISM: Homo sapiens	Query Match 3.5%; Score 81; DB 7; Length 607; Best Local Similarity 19.4%; Pred. No. 15; Pred. No. 15; Pred. S0; Mismatches 137; Indels 196; Gaps 27; Qy 81 LQSFRLGCANLKORROGWODVCAQAFOTPVHSFQAKQFFERYFTPWQV 127

Qy 386NRLIMAQDTGSAIDGAVRUDYFWGYĞDBAGBLAGKQKTTGYVWQLLPNG 434	SULT 19 Sequence 51, Application US/11113424 Publication No. US20050260713A1 APPLICANT: Gangolli et al. APPLICANT: Gangolli et al. TITLE OF INVENTION: Polybebtides and Nucleic Acids Encoding Same	3, 424	Query Match 3.5%; Score 81; DB 7; Length 2715; Best Local Similarity 18.7%; Pred. No. 1.2e+02; Matches 89; Conservative 49; Mismatches 140; Indels 198; Gaps 23;	Qy 81 LQSFRLGCANLKORQGWQDVCAQAFQTPVHSFQAKQFFERYFTPWQV 127	QY 128 AGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187	Qy 188 GKNSGTIDNTGGTHTADLSRFPITARTTA-IKGRFEGSRFL-PYHT	Qy 232MHIQGSGRLK 268 Qy	Qy 269 TPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ-327 	Qy 328 NPSYIFFRELAGSSNDGPVG 347 :	Qy 348 ALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKAL 385 Qy 1114 ELDASNMGGWTLDKHHVLDVQNGILYKGNGENQFISQQPPVVSSIMGNGRRRSISCPS 1171
OY 328PDSYIFFRELAGSSNDGPVGALGTPLMGE 356 Db 714 I-POKWFDASDMIAVPRIMDKTHAVNOKYNSVGSVGSVGSCT.DI.TI.WEVGTAIT.OG 773	357 Y	RESULT 18 US-11-096-051-2 Sequence 2, Application US/11096051 Sequence 2, Application WS/11096051 Sequence 2, Application No. US20050244868A1 Sequence 2, Application No. US20050244868A1 SENDICANT: Media, Ramesh APPLICANT: Mediachan, Timothy K APPLICANT: Mediachan, Timothy K APPLICANT: Ratelaberg, Seth TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use FILE REFERENCE: Attorney Docket No. Cura 967 CURRENT FILING DATE: 2006-03-30 FRIOR APPLICATION NUMBER: 10/038,854 FRIOR APPLICATION NUMBER: 10/038,854 FRIOR APPLICATION NUMBER: 10/038,854 FRIOR APPLICATION NUMBER: 60/557,978 FRIOR APPLICATION NUMBER: 60/557,978 FRIOR APPLICATION NUMBER: 60/557,978 FRIOR APPLICATION NUMBER: 60/557,978 FRIOR APPLICATION NUMBER: 60/557,978 FRIOR APPLICATION NUMBER: 60/557,978 FRIOR PILING DATE: 2004-03-30 NUMBER OF SEQ ID NOS: 38 SOFTWARE: CuraSeqList version 0.1 SEQ ID NO 2 LENGTH: 2715 TYPE: PRT TYPE: PRT	Query Match 3.5%; Score 81; DB 7; Length 2715; Best Local Similarity 19.4%; Pred. No. 1.2e+02; Matches 92; Conservative 50; Mismatches 137; Indels 196; Gaps 27;	QY 81 LQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFERYFTPWQV 127	QY 128 AGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187	QY 188 GKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFL-PYHT	OY 232RNQINGGALDGKAPILGYAEDPVELFFMHIQGSGRL 267 Db 951 LVMKKEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSSPEDSPIIPETQVLHEE 1003	OY 268 KTPSGKYIRIGYADKONEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ 327	Qy 328NPSYIFFRELAGSSNDGPVGALGTPLMGE 356 Db 1053 LFQKWPPASPNLAYTFIWDKTDAYNQKVYGLSEAVVSVGYEYESCLDLTLWEKRTAILQG 1112	Qy 357 YAGAVDRHYITLGAPLFVATAHPVTRKAL 385

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Sequence 8, Application US/11096051
Publication No. US20050244868A1
GENERAL INFORMATION:
APPLICANT: Retuda, Ramesh
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Retude, Corine
APPLICANT: Retenberg, Seth
TILE OF INVENTION: Ten-M3 Polypeptides and Polymucleotides and their Methods of Use
FILE REFERENCE: Attorney Docket No. Cura 967
CURRENT FILING DATE: 2005-03-30
FILE REFERENCE: 2001-12-31
PRIOR FILING DATE: 2001-12-31
PRIOR FILING DATE: 2003-06-04
PRIOR PLING DATE: 2003-06-04
PRIOR PLING DATE: 2004-03-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Curasequist version 0.1
SEQ ID NO 8
LENGTH: 2725
LENGTH: 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 19.4%,
Matches 92; Conservative
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                                                                                                                                                                      ## Sequence 10, Application US/11096051

| Sequence 10, Application US/11096051
| Publication No. US20050244868A1
| Sequence 10, Application No. US20050244868A1
| APPLICANT: Kekuda, Ramesh
| APPLICANT: Rastelli, Luca
| APPLICANT: Rastelli, Luca
| APPLICANT: Rastelli, Luca
| APPLICANT: Ettenberg, Seth
| TITLE OF INVENTION: Ten-May Polypeptides and Polynucleotides and their Methods of Use
| TITLE OF INVENTION: Ten-May Polypeptides and Polynucleotides and their Methods of Use
| TITLE OF INVENTION: Ten-May Polypeptides and Polynucleotides and their Methods of Use
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| TITLE OF INVENTION: Ten-May Polypeptides and Polynucleotides and their Methods of Use
| TITLE OF INVENTION NUMBER: US/11/096,051
| PRIOR PILING DATE: 2003-06-04
| PRIOR PILING DATE: 2003-06-04
| PRIOR PILING DATE: 2004-03-30
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: CuraSequist version 0.1
| SEQ ID NO 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 KTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                873 PFNKSLASVIRG---QVLTADGT-----PLIGVNVSFFHYP-----EYGYTITR---- 913
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----NYVRRIFPSG 1210
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                                ----NRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVWQLLPNG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.5%; Score 81; DB 7; Length 2721; Best Local Similarity 19.4%; Pred. No. 1.2e+02; Matches 92; Conservative 50; Mismatches 137; Indels 196;
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ORGANISM: Homo sapiens
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US-11-096-051-8
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.014 TTIPGTDLKLSYLSSRAAGYKSV------LKI--TWTQSIIPFNLMKVHLMVAVVGR 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1123 YELDASNMGGWTLDKHHVLDVQNGILYKGNGENQFISQQPPVVSSIMGNGRRRSISCPSC 1182
                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 KTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ 327
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                                                                                                                                                                                                        821 LQS----SCONOPYCRGLPDPQDIISOSLOSPSQQ-AAKSFYDRISFLIGSDSTHVIPGES 876
                                                                                                                                                                                                                                                                            128 AGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187
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---NYVRRIFPSG 1220
3.5%; Score 81; DB 7; Length 2725;
19.4%; Pred. No. 1.2e+02;
tive 50; Mismatches 137; Indels 196; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVWQLLPNG
                                                                                                                                                                                                                                                                                                                                                                                                                    188 GKNSGTID--NTGGTHTADLSRFPITARTTAIKGRFEGSRFL-PYHT-----
                                                                                                                                           81 LQSFRLGCANLKNRQGW---QDVCAQAFQTPVHSFQAKQFFER-
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
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36; Gaps

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221 FEGSRFLP----YHTRNQINGGA-----LDGKAPILGYAEDPVELFFMH--IQGSGRLKT 269
                                                                                                                                                                                                      126 NNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVG-MHI 184
                                                                                                                                                                                                                                                        270 PSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQNP 329
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR PLING DATE: 1997-08-26
PRIOR PLING DATE: 1997-09-17
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333001C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
                                                    169 VPLPAGLRSGKALVRIR----QTGKNSGTIDNTGGTHTADLSRFPITAR---TTAIKGR
                                                                                                                                                                                                                                                                                                                                                             330 SYIFFRELAGSSNDGPVGAL-GTPLMGEYAGAVDRHYITLGAPLFVATAHPV 380
                                                                                                                                                                                                                                                                                                                                                                                                          -----NGHVGAIAGDNALKAKAGETVRMÝVGNGGPNLVSSFHVI 282
       33; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 144, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Gurney, Austin L.
     52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard, Audrey
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CORGANISM: Homo Sapien
US-10-131-826A-144
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LENGTH: 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNAGTVKGNG-----EH----HWKTTGTNSHIGSTAVRLANNEGDANNGQNVTFEDNG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 TLVLDQNINQGAGGLFFKGDYTVKGANNDITWLGAGIDVADGKKVVWQVKNPNGDRLAKI 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 GKGTLEINGTGVNQGQLKVGDGTVILNQKADSNQKVQA-FSQVGIVSGRGTLVLNSPDQI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 ISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRF 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 IRIGYADKNEHPYV----SIGRYMADKG-----YLKLGQTSMQGIKSYM-RQNPQRLA 322
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                                                                                                                                                                                                                                                                                                                                                                                                          40; Mismatches 140; Indels 143;
                                                                                                                                                                                                                                                                                                                                                             Length 1565;
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Pred. No. 15;
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: PASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTON: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                        Query Match
3.4%; Score 79.5; DB 6;
Best Local Similarity 21.2%; Pred. No. 77;
Matches 87; Conservative 40; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AQAFQTPVHSFQAKOFFERYFT------
                                             CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                            PRIOR APPLICATION NUMBER: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 2704
LENGTH: 1565
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1784
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
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SEQ ID NO 1784
LENGTH: 392
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Best Local Similarity
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APPLICANT: Kulowski, Kerry
APPLICANT: Fulowski, Kerry
APPLICANT: Pong, Kevin
TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
TITLE OF INVENTION: Bolyketide
FILE REFERENCE: AM-101426US
CURRENT APPLICATION NUMBER: US/11/143,980
CURRENT APPLICATION NUMBER: US 60/644,483
PRIOR PILING DATE: 2005-03-23
PRIOR FILING DATE: 2005-03-23
PRIOR FILING DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 VGGGGAVYTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AKQFFERYF------TPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQAR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2774, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICART: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPRENCE: PUJ486US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SGOTWARE: Patentin Ver. 2.1
SEQ ID NO 2774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 FRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTT
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                                           364 AGRQAARVAIYRMMRPGEPP 383
                                                                                                                                                                                     Sequence 47, Application US/11143980
Publication No. US20050272133A1
GENERAL INFORMATION:
        418 AGKOKTTGYVWQLLPNGMKP 437
                                                                                                                                                                                                                                                          APPLICANT: He, Min
APPLICANT: Hucul, John
APPLICANT: Haltli, Bradley A.
APPLICANT: Haltli, Bradley A.
APPLICANT: Graziani, Edmund
APPLICANT: Summers, Mia
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                                                                                                                                                                                                                                                                                                                                                       ...-----KALAADLIDSETGEV-----L 317
                                                                                                                                                            52 KAPTSTRFSDAIRAFQWVSQLPVSGVLDRATLRQMTRPRCGVTDTNS--YAAWAERISDL 109
                                                                                                                                                                                                                -----KGYLKLGQTSMQGIKSYMRQN-PQRLAE-----VLGQNPSYIF 333
                                                                                                                                                                                                                                                               110 FARHRIKMRRKKRFAKQGNKWYKQHLSYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALE 169
                                                                                                                                                                                                                                                                                                                      334 FREL----T----T 367
                                                                                                                                                                                                                                                                                                                                                                                                                            368 LGAPLFVATAHPV----TRKALNRLIMA------QDTGSAIDGAVRVDYFWGY---G 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 RGRNLFVVLAHEIGHTLGLTHSPAPRALMAPYYKRLGRDALLSWDDVLAVQSLYGKPLGG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 VPL--PAG--LRSGKALVRIRQTGKNSGTI--DNTGGTHTADLSRFPITARTTAIKGRFE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 GSRFLPYHTRNQINGGALD----- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SARIIPY-----RGSWLDFEFDPKDLLYFRIDRRRKMPVTILLKALGYNNEQILDIFYD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LKLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAVDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIDGAVRVDYFWGYGDEAGEL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 ASANDEITEELLAKFDINGVKEITTLYINEL----DQGAYİSNTLRTD------ET 363
                                                                                                           243 KAPILGYAEDPVELF--FMHIQGSGRLKTPSGKYI----RIGYADKNEHPYVSIGRYMAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 -ELFFMHIQG-----SGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGY----
                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 7930. Application US/10467657
sequence 7930. Application US/10467657
sequence 7930. Application US/10467657
sequence 7930. Application US/20000260581A1
sequence 7930. Application No. US20000260581A1
sequence 7930. Application Spa
sequence 7930. Application Spa
sequence 7930. Application Application Application MonAct Elisabetta
sequence 7930. Application NUMBER: US/10/467,657
sequence 7930. Application NUMBER: GB-0103424.8
sequence 7930. NUMBER: GB-0103424.8
sequence 7930. NUMBER OF SEQ ID NOS: 9218
sequence 7930. Sequence 7930. LENGTH: 1394
septime 7394.
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3.3%; Score 78; DB 6; Length 520;
23.9%; Pred. No. 23;
tive 23; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 78; DB 6
19.7%; Pred. No. 89;
tive 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 DEAGELAGKOKTTGYVW-QLLPNGMKPE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 SVAVQLPGKLFTDFETWDSYSPQGRRPE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 TRLDVEOESLLG----
Query Match
Best Local Similarity 23.9%
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Conservative
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Best Local Similarity
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131 ---GSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187
                                                                                                                                                                                                                                                                                                   249 TLVGSMQDAVTGYMLTAL----ARLGDALF-------LTAGIVVG-ILISLR-- 288
                                                                                                                                                                                                                                                                                                                                                                    188 GKNSGTIDNTGGTHTADLSRFPITARTT-AIKGRFEGSRFLPYHTRNQINGGALDGKA-P 245
                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GVTNAGIQIELHVDATTTLATPG------MPLPILVAVSGAALSGVCLT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 ILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 IASYAP-----LRSVATAGLSAGLAE----LUGLGAAGFGRVVATWT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 SMQGIK-----SYMRONPQRLAEVLGQNPSY----IFFRELAGSSNDGPVG----- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 AAIGVGFLATLISIRRQAPALVTATAGIMPMLPGLAVFRAVFAFAVNDTPDGGLTQLLEA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 GGVAVDQAHBAMDELTERPH-PYPRWLA---TAGAAGFALGVAMILG--GTWLTCVLAAV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 TSGVIDRLGRLLNRIGTPLFFQRVFGAGIATLVAVAAYLIAGQDPTALVATGIVVLLSGM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQT 187
                                                                                                                                                             189 İSGVIDRLGRLLINRIGTPLFFQRVFGAGIATLVAVAAYLIAĞQDPTALVATGIVVLLSGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAV-----YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 TP-----VHSFQAKQFFERYF-----TPWQVAGN-------
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| APPLICANT: Balley, Richard B. |
| APPLICANT: Balley, Richard B. |
| APPLICANT: Blomquist, Paul B. |
| APPLICANT: Driggers, Edward M. |
| APPLICANT: Driggers, Edward M. |
| APPLICANT: O'Icary, Jessica BAPLICANT: O'Icary, Jessica BAPLICANT: Trucheart, Joshua APPLICANT: Trucheart, Joshua APPLICANT: Trucheart, Joshua APPLICANT: Trucheart, Joshua APPLICANT: Trucheart, Joshua BAPLICANT: POTGEY, Peter S. |
| APPLICANT: POTGEY, Peter S. |
| APPLICANT: POTGEY, Peter S. |
| TITLE OF INVENTION: PRODUCTION FILE OF INVENTION: PRODUCTION |
| FILE REFRENCE: 14184-33001 |
| CURRENT APPLICATION NUMBER: US 60/475,000 |
| PRIOR APPLICATION NUMBER: US 60/551,860 |
| PRIOR APPLICATION NUMBER: US 60/551,860 |
| NUMBER OF SEQ ID NOS: 364 |
| SOFTWARE: PSSEC OF Windows Version 4.0 |
| FEBRICANT: FOR SEC OF WINGOWS VERSION 4.0 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105, Application US/10858730 Publication No. US20050255568A1 GENERAL INFORMATION:
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US-10-858-730-105
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                                                                                                                                                                                                                                                                                                                                                                                                          61 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKORQGWQDVCAQAFQTPVH-SFQAKQFFE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ------QPF--SLEKILLGGAKLSPQLIEQ---ALTYRLPVYNSFGWTETCS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SPQMLKERFDTVGKPSENVEVKIKNPNAYGH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKALVRIRQTGKN-----SGTIDNTGGTHTADLSRFPITARTTAIKGRFE---- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GGENIYPY----QIETIAKDFEGIEDAVCVGISDDTWGQVPILYYVTNQDINQTELIEHF 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 RYFTPWOVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPL--PAGLRS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GKAPILGYAEDP-----VELF 257
                                                                                                                                                                                                                                                                                                                                                                 5 LFRAALYGIAAAILAACQS----KSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV 60
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al Similarity 22.2%; Pred. No. 26;
92; Conservative 35; Mismatches 151; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                            ) OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
US-10-793-626-2774
                                                                                                                                                                                                                                                                                                   Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOHERANI INFORMATION:
JAPPLICANT: Blomquist, Paul
APPLICANT: Blomquist, Paul
APPLICANT: Blomquist, Paul
APPLICANT: Driggers, Edward M.
APPLICANT: Driggers, Edward M.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: Trueheart, Joshua
APPLICANT: Walbridge, Michael J.
APPLICANT: Walbridge, Michael J.
APPLICANT: Walbridge, Michael J.
APPLICANT: Worgey, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 14184-030001
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR PILING DATE: 2004-06-01
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 104
                                                                                                                                                                                                                                     Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 FMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 77.5; DB 6; Best Local Similarity 20.6%; Pred. No. 17; Matches 70; Conservative 37; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 104, Application US/10858730
Publication No. US20050255568A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 -GSRFLPYHTRNQINGGALD
TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 92; Conserv;
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                                                                        FEATURE:
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Job time : 12

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2101 DIQTEDLEDGTCKVSYFPTVPGVYIVSTKFADEHVPGSPFTVKISGEGRVKESITRTSRA 2160
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Sequence 1262, Application US/10821234

Sequence 1262, Application US/10821234

Sequence 1262, Application US/10821234

Sequence 1262, Application US-1082055114A1

Sequence 1262, Application US-108205

APPLICANT: Labat, Ivan

APPLICANT: Labat, Ivan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PLESC_Genes Version 1.0

SEQ ID NO 1262

LENGTH: 2657
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-----LTAGIVVG-ILISLR-- 288
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                                                            GKNSGTIDNTGGTHTADLSRFPITARTT-AIKGRFEGSRFLPYHTRNQINGGALDGKA-P 245
                                                                                      ILGYAEDPVELFFWHIQGSGRLKTPSGKYIRIGYADKWEHPYVSIGRYMADKGYLKLGQT 305
                                                                                                                                                                                                                  306 SMQCIK-----SYMRQNPQRLAEVLGQNPSY----IFFRELAGSSNDGPVG----- 347
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                                                                                                                                                                                                                                                                                            ----ALGT-PLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGS 396
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20.1%; Pred. No. 2.4e+02;
tive 39; Mismatches 101; Indels 143;
249 TLVGSMQDAVTGYMLTAL----ARLGDALF----
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Best Local Similarity 20.1*
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ORGANISM: Homo sapiens
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Search completed: December 30, 2005, 08:28:54

14, Appl 12009, A 4, Appli 10113, A 54065, A 253747,

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GENERAL INFORMATION:
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APPLICANT: Frazer, Claire M.
APPLICANT: Peterson, Jeremy
APPLICANT: Peterson, Jeremy
APPLICANT: Tettelin, Herve
APPLICANT: Venter, J. Craig
APPLICANT: Wasignani, Vega
APPLICANT: Masignani, Vega
APPLICANT: Masignani, Marios
APPLICANT: Ratti, Giulio
APPLICANT: Scarselli, Maria
APPLICANT: Scarselli, Maria
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APPLICANT: Scarselli, Maria
APPLICANT: Galecti, Giulio
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Brandi, Guido
APPLICANT: Brandi, Guido
TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
FILE REFERENCE: 0244-08-11
PRIOR PPLICATION NUMBER: US/806,866
PRIOR FILING DATE: 1999-10-09
PRIOR PILING DATE: 1999-10-09
PRIOR PILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
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US-10-282-122A-54065
US-10-282-122A-54065
US-10-282-122A-54065
US-10-282-122A-64807
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Matches 440; Conservative
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Sequence 995, App
Sequence 14, Appl
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(GGTZ 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
(GGTZ 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
(GGTZ 6/ptodata/1/pubpaa/USOA_PUBCOMB.pep:*); (GGTZ 6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*); (GGTZ 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*); (GGTZ 6/ptodata/1/pubpaa/USII_PUBCOMB.pep:*);
                          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-484-218-22
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US-10-220-481-1
US-10-121-456A-1
US-10-121-456A-1
US-10-212-456A-1
US-10-212-456A-99
US-10-21-481-3
US-10-220-481-3
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                                                                                           DGKAPILGYAEDPVELFFWHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL 300
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TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
FILE REFERENCE: P023783W0
CURRENT APPLICATION NUMBER: US/10/181,660
CURRENT FILING DATE: 2003-03-31
PRIOR PILIAGION NUMBER: GB-0001067.8
PRIOR PILING DATE: 2000-01-17
PRIOR PILING DATE: 2000-01-17
PRIOR PILING DATE: 2000-01-17
PRIOR FILING DATE: 2000-01-17
PRIOR FILING DATE: 2000-01-17
PRIOR FILING BATE: 2000-01-17
PRIOR FILING SEQ ID NOS: 14
SOFTWARE: SEGWIN99, version 1.02
SEQ ID NO 14
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; Publication No. US20030027097A1
; GENERAL INFORMATION:
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ORGANISM: Neisseria meningitidis
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Best Local Similarity
Matches 439; Conserv
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APPLICANT: Masignant, vega
APPLICANT: Ratti, Giulio
APPLICANT: Ratti, Giulio
APPLICANT: Ratti, Giulio
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Thei
FILE REFERENCE: 002441.0009
CURRENT FILING DATE: 2004-08-11
PRIOR PILICATION NUMBER: US/10/915,740A
CURRENT FILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1068
NUMBER OF SEQ ID NOS: 1068
SOFTWARE: PATENTIN VERSION 3.2
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ORGANISM: Neisseria meningitidis
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APPLICANT: Hickey, Erin
APPLICANT: Peterson, Jeremy
APPLICANT: Tettelin, Herve
APPLICANT: Wenter, J. Craig
APPLICANT: Masignani, Vega
APPLICANT: Mora, Manrosa
APPLICANT: Ratti, Giulio
APPLICANT: Scarielli, Maria
APPLICANT: Scarielli, Maria
APPLICANT: Scarielli, Maria
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APPLICANT: Rappuoli, Rino
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                            KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
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TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins FILE REFERENCE: CHR-15883/01US
CURRENT APPLICATION NUMBER: US/10/220,481
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: PCT/IB01/00452
PRIOR PLING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 633
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 1
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llarity 99.5%; Pred. No. 1.8e-214;
Conservative 1; Mismatches 1; Indels
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ORGANISM: Neisseria meningitidis
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US-10-220-481-1
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APPLICANT: MOE, Gregory
APPLICANT: MOE, Gregory
APPLICANT: RAPPOLI, R.
INCOMPLICANT: RAPPOLI, R.
ITLE OF INVENTION: MOLECULAR MIMETICS OF MENINGOCOCCAL B EPITOPES WHICH
ITLE OF INVENTION: ELLCIT FUNCTIONALLY ACTIVE ANTIBODIES
FILE REFERENCE: 2302-17782 / PP17782.03
FILE REFERENCE: 2302-17782 / PP17782.03
CURRENT APPLICATION NUMBER: US/10/121,456A
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATENTIN VET. 2.0
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                                                                            APPLICANT: CHIRON SpA
TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
FILE REFERENCE: P023795WO
CURRENT APPLICATION NUMBER: US/10/181,600
CURRENT APPLICATION NUMBER: GB-0001067.8
PRIOR APPLICATION NUMBER: GB-0005699.4
PRIOR FILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: GB-0005699.4
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 14
LENGTH: 441
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; Sequence 14, Application US/10181600; Publication No. US20040249125A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Neisseria meningitidis US-10-181-600-14
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us-09-914-454b-31.rapbm

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APPLICANT: Pizza, Mariagratia
APPLICANT: Pizza, Mariagratia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
THE REFERENCE: 002441.00090
CURRENT APPLICATION NUMBER: 2004-08-11
                                                                                                                                                                                                   1 MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
                                                                                                                                                                                                                                                                                                                                                                                     LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
                                                                        OTHER INFORMATION: Description of Artificial Sequence: exemplary GNA33 OTHER INFORMATION: sequence
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                                                                                                                                   Score 2302; DB 4; Length 441;
Pred. No. 9e-212;
3; Mismatches 4; Indels
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PRIOR APPLICATION NUMBER: 09/806,866
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 999, Application US/10915740A; Publication No. US20050191316A1; GENERAL INFORMATION:
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Peterson, Jeremy
Tettelin, Herve
Venter, J. Craig
Masignani, Vega
Galeotti, Cesira
Mora, Manrosa
Ratti, Giulio
Scarselli, Maria
Scarlato, Vincenzo
Rappuoli, Rino
                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                    98.4%;
ilarity 98.4%;
Conservative
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                                                                                                                                                    Similarity
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Best Local Simi
Matches 434;
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SEQ ID NO 1
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TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
FILE REFERENCE: CHIR-15883/01US
CURRENT APPLICATION NUMBER: US/10/220,481
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: PCT/IB01/00452
PRIOR FILING DATE: 2001-06-28
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98.4%; Score 2302; DB 5; Length 441;
Best Local Similarity 98.4%; Pred. No. 9e-212;
Matches 434; Conservative 3; Mismatches 4; Indels
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PRIOR APPLICATION NUMBER: USSN 60/132,068
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 1068
SOFTWARE: PatentIn version 3.2
SEQ ID NO 999
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                                                                                                                                                                                                                                                    , ORGANISM: Neisseria meningitidis
US-10-915-740A-999
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SOFTWARE: SegWin99, version 1.02
SEQ ID NO 3
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Best Local Similarity
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TYPE: PRT
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APPLICANT: Peterson, Jagemy
APPLICANT: Tettelin, Herve
APPLICANT: Tettelin, Herve
APPLICANT: Tettelin, Herve
APPLICANT: Tettelin, Herve
APPLICANT: Galecti, Cesira
APPLICANT: Galecti, Cesira
APPLICANT: Galecti, Cesira
APPLICANT: Rati, Giulio
APPLICANT: Rati, Giulio
APPLICANT: Scarselli, Maria
APPLICANT: Scarselli, Maria
APPLICANT: Rappouli, Rino
APPLICANT: Rappouli, Rino
APPLICANT: Rappouli, Rino
APPLICANT: Bizza, Mariagratia
APPLICANT: Bizza, Mariagratia
APPLICANT: Bizza, Mariagratia
APPLICANT: Bizza, Mariagratia
APPLICANT: Pizza, Mariagratia
APPLICANTON NUMBER: US/10/915, 740A
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 1068
SOFTWARE: PatentIn version 3.2
SECTOR NO 4097
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                                         3 KYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAVYT
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      Gaps
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    11; Indels
  1; Mismatches
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; ORGANISM: Neisseria gonorrhoeae
US-10-915-740A-997
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  Conservative
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US-10-915-740A-997
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TITLE OF INVENTION: Hybrid Expression of Neisserial Proteins
FILE REFERENCE: PO26783M
CURRENT APPLICATION NUMBER: US/10/220,480
CURRENT PILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: GB 0004695.3
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-10-13
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                                 Indels
   Length
Query Match 96.5%; Score 2257; DB 5; Best Local Similarity 95.7%; Pred. No. 1.9e-207; Matches 422; Conservative 9; Mismatches 10;
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; OTHER INFORMATION: deltaG287-919
US-10-220-480-4
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SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 4
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Matches 419; Conservative
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US-10-220-480-4
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US-10-220-480-10
i Sequence 10, Application US/10220480
i Publication No. US20040092711A1
i GENERAL INFORMATION:
i APPLICANT: Chiron SpA
i TTILE OF INVENTION: Hybrid Expression of Neisserial Proteins
i TILE REFERENCE: P026783WO
i CURRENT FPLICMTION NUMBER: US/10/220,480
i CURRENT FILING DATE: 2000-02-28
i PRIOR APPLICATION NUMBER: GB 0004695.3
i PRIOR FILING DATE: 2000-02-28
i PRIOR FILING DATE: 2000-01-28
i PRIOR FILING DATE: 2000-01-28
i RIOR APPLICATION NUMBER: GB 0027675.8
i RIOR APPLICATION NUMBER: 2000-01-13
i NUMBER OF SEQ ID NOS: 121
i SOFTWARE: SeqWing9, version 1.02
i LENGTH: 897
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95.6%; Score 2236; DB 4;
Best Local Similarity 99.5%; Pred. No. 5.4e-205;
Matches 419; Conservative 1; Mismatches 1;
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ORGANISM: Artificial Sequence
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                                                                                              HTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPILGYAEDPVELFFMH 260
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US-10-220-481-89
; Sequence 89, Application US/10220481
; Sequence 89, Publication No. US200401106/00A1
; GENERAL INFORMATION:
; APPLICANT: ARICO, MATIA B., et al.
; TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
; TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
; CURRENT APPLICANION NUMBER: US/10/220,481
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/1B01/00452
; RIOR RILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 633
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 89
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Pred. No. 4.8e-205;
1; Mismatches 1;
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OTHER INFORMATION: deltaG287-919
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Best Local Similarity 99.5%;
Matches 419; Conservative
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US-10-220-481-89
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Sequence 95, Application US/10220481
; Bublication No. US20040110670A1
; GENERAL INFORMATION:
    APPLICANT: ARICO, Maria B., et al.
    TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
    FILE REFERENCE: CHIR-15883/01US
; CURRENT APPLICATION NUMBER: US/10/220,481
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/IB01/00452
; RIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 633
; SOFTWARE: SeqWin99, version 1.02
; FEG ID NO 95
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TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
FILE REFERENCE: CHIR-15883/0105
CURRENT APPLICATION NUMBER: U$/10/220,481
PRIOR APPLICATION NUMBER: PCT/IB01/00452
PRIOR RILING DATE: 2001-02-28
NUMBER OF SEO ID NOS: 633
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Best Local Similarity 99.5%; Pred. No. 5.4e-205;
Matches 419; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                        , OTHER INFORMATION: deltaG287NZ-919
US-10-220-481-95
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US-10-220-481-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 RKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGKQKTTGYVWQLLPNGMKPEYRP 420
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Sequence 8, Application US/10220481

Sequence 8, Application US/10220481

Publication No. US20040110670A1

GENERAL INFORMATION:

APPLICANT: ARICO, Maria B., et al.

TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins

FILE REFERENCE: CHIR-15883/01US

CURRENT APPLICATION NUMBER: US03-05-05

PRIOR APPLICATION NUMBER: PCT/1B01/00452

PRIOR APPLICATION NUMBER: PCT/1B01/00452

NUMBER OF SEQ ID NOS: 633

SOFTWARE: SeqWin99, version 1.02

SEQ ID NOS:
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Pred. No. 9.3e-89;
0; Mismatches 1; Indels (
                                                                                                                                                           Length 420;
                                                                                                                                                                                                         Indels
                                                                                                                                                      95.2%; Score 2227; DB 4;
99.5%; Pred. No. 1.3e-204;
iive 1; Mismatches 1;
; SEQ ID NO 2
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-220-481-2
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Similarity 99.5%;
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Best Local Similarity 99.5'
Matches 193; Conservative
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US-10-220-481-8
                                                                                                                                                                                 Best Local Similarity 99.5
Matches 418; Conservative
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GENERAL INFORMATION:
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                     GAVDRHYITLGAPLFVATAHPVTRKALNRLIMAQDIGSAIKGAVRVDYFWGYGDEAGELA 180
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GAVDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELA 418
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                                                                                                                                                                                             Sequence 2, Application US/10415017
; Sequence 2, Application US/10415017
; Publication No. US20040043456A1
; GABERAL INFORMATION:
    APPLICANT: Thomazd, Joelle
; TITLE OF INVENTION: BASB209 Polypeptides and Polynucleotides
; TITLE OF INVENTION: From Haemophilus Influenzae
; TITLE OF INVENTION: from Haemophilus Influenzae
; URRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: PCT/EP01/12391
; PRIOR APPLICATION NUMBER: GB 0025997.8
; PRIOR APPLICATION NUMBER: GB 0025997.8
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.5%; Score 316.5; DB 4; 24.5%; Pred. No. 2.6e-21; iive 58; Mismatches 142;
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ORGANISM: non-typeable Haemophilus influenzae
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                                                                                                GKOKTTGYVWQLLP 194
                                                                         GKOKTTGYVWOLLP 432
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Matches 117; Conservative
                                                                                                                                                                  RESULT 16
US-10-415-017-2
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; Sequence 6, Application US/10415017; Publication No. US20040043456A1

RESULT 17 US-10-415-017-6

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262 RNEAYVFFK-----NDPSGKVKGSAGVPLVAMASVASDRNIIPSGSVLLVEVPDIDNNG 315
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Publication No US20040043456A1

GENERAL INFORMATION:

APPLICANT: Thornard, Joelle

TITLE OF INVENTION: BASB209 Polypeptides and Polynucleotides

TITLE OF INVENTION: BASB209 Polypeptides and Polynucleotides

FILE REFERENCE: BM45427

CURRENT APPLICATION NUMBER: US/10/415,017

CURRENT PILING DATE: 2003-04-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Thonnard, Joelle
TITLE OF INVENTION: BASB209 Polypeptides and Polymucleotides
TITLE OF INVENTION: BASB209 Polypeptides and Polymucleotides
TITLE OF INVENTION: BASB209 Folypeptides and Polymucleotides
FILE REFERENCE: BM45427
CURRENT PILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: POT/FEP01/12391
PRIOR PILING DATE: 2001-10-24
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.5%; Score 316.5; DB 4; Best Local Similarity 24.5%; Pred. No. 2.6e-21; Matches 117; Conservative 58; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: non-typeable Haemophilus influenzae
US-10-415-017-6
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144 ARHSPQGQFKNPIYRMP----
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109 VHSFQAKQFFERY--FTPWQVAG--
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145 RHSPQG@FKNPIYRMP---
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                                                                                                Query Match 13.5%; Score 316.5; DB 4; Length 367; Best Local Similarity 24.5%; Pred. No. 2.6e-21; Matches 117; Conservative 58; Mismatches 142; Indels 161;
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; Publication No. US20040043456A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THORDARY JOSHLE
; TITLE OF INVENTION: BASB209 POlypeptides and Polynucleotides
; TITLE OF INVENTION: Erom Haemophilus Influenzae
; FILE REFERENCE: BM45427
; CURRENT APPLICATION NUMBER: US/10/415,017
; CURRENT FILING DATE: 2003-04-24
; PRIOR PAPLICATION NUMBER: PCT/EPO1/12391
; PRIOR PELICATION NUMBER: GB 0025997.8
; PRIOR APPLICATION NUMBER: GB 0025997.8
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FESTEREQ for Windows Version 4.0
; SEQ ID NO 8
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                                 ; TYPE: PRT
; ORGANISM: non-typeable Haemophilus influenzae
US-10-415-017-10
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, ORGANISM: non-typeable Haemophilus influenzae
US-10-415-017-8
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Best Local Similarity
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US-10-415-017-8
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SEQ ID NO 10
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YT-----VVPHLSLPHWAA----QDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTP 108
                                                                                                                            ------NGSLAGTVTGYYEPVLKG 147
                                                                                                                                                                                        85 YSSKLSTNFYDNYEKITNWVLSGANINELTQFNIQPQIMRGFDGFQNVLMTGYYSPILYA 144
                                                                                                                                                                                                                                                        148 DDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSR 207
                                                                                                                                                                                                                                                                                                                     208 FPITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPILGYAEDPVELFFMHIQGSGRL 267
                                                                                                                                                                                                                                                                                                                                                                                                                         268 KTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 NEAYVFFK-----NDPSGKVKGSSGVPLVAMASVASDHNIIPSGSVLLVEVPDIDNNGN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YT-----VVPHLSLPHWAA----QDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTP 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 YSSKLSTNFYDNYEKITNWVLSGANINELTQFNIQPQIMRGFDGFQNVLMTGYYSPILYA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 DDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 ---AHPVTRKALNRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVWQL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomnard, Joelle
TITLE OF INVENTION: BASBASO Polypeptides and Polynucleotides
TITLE OF INVENTION: from Haemophilus Influenzae
FILE REFERENCE: BM45427
CURRENT APPLICATION UNMBER: US/10/415,017
CURRENT FILING DATE: 2003-04-24
PRIOR PLILING DATE: 2003-04-24
PRIOR FILING DATE: 2000-10-24
PRIOR PLILING DATE: 2000-10-24
PRIOR PLILING DATE: 2000-10-24
                                        , ORGANISM: non-typeable Haemophilus influenzae US-10-415-017-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 367
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us-09-914-454b-31.rapbm

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Matches
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                         203 DFGDGNLNYFAYAGQNGYPYTAIGRLLVEDGEIPKEKMSIQAIREWSNRNPSRVQSLLER 262
                                                                                                                                                                           263 NEAYVFFK-----NDPSGKVKGSSGVPLVAMASVASDHNIIPSGSVLLVEVPDIDNNGN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 TSMQGIKSYMRQNPQ-RLAEVLGQNPSYIFFRELAGSSNDGPV-GALGTPLMGEYAGAVD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHYITLGAPLFVATAHPVTRKALN-----RLIMAQDTGSAIDGAVRVDYFWGYGDEAGEL 417
                                                                         268 KTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ 327
                                                                                                                                                   328 NPSYIFFRELAGSSND--GPV-GALGTPLMGEYAGAVDRHYITLGAPLFVAT----- 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FPITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPILGYAEDPVELFFMHIOGSGRL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 ---AHPVTRKALNRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVWQL 430
                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10220481

Publication No. US20040110670A1

GENERAL INFORMATION:

APPLICANT: ARICO, Maria B., et al.

TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
FILE REFERENCE: CHIR-15883/01US

CURRENT APPLICATION NUMBER: US/10/220,481

CURRENT FILING DATE: 2003-05-05

PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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Sequence 54683, Application US/10450763

Sequence 54683, Application US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

INTUNE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CTP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-03-31

PRIOR PLING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 238.5; DB 4; Length : larity 35.2%; Pred. No. 3.2e-14; Conservative 25; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 633
SOFTWARE: SegWin99, version 1.02
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Escherichia coli
US-10-220-481-9
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Best Local S
Matches 68
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eMATRIX,
raw score of 26.50
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NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
DOCATION: (670)..(718)
OTHER INFORMATION: CHEMOTAXIS CHEW PROTEIN domain identified by eMATRIX,
OTHER INFORMATION: accession number DM01794, p-value=1.000e-40, raw score of
FEATURE:
NAME/KEY: DOWAIN
LOCATION: (664)..(803)
OTHER INFORMATION: CheW-like domain identified by PFam, accession name CheW,
OTHER INFORMATION: value=6.5e-53, PFam score of 189.2
FEATURE:
NAME/KEY:
NAME/KEY:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 FFMHIQGSGRLKTPSGKYIR-IGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 FIMDVQGSGYIDFGDGSPLNFFSYAGKNGHAYRSIGKVLIDRGEVKKEDMSMQAIRHWGE 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 VATAHPVTRKALN-----RLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVW 428
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OTHER INFORMATION: FAD binding domain identified by PFam, accession name
OTHER INFORMATION: FAD_binding_2, E-value=5.6e-21, PFam score of 76.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 QNPQ-RLAEVLGQNPSYIFFRELAGSSNDGPV-GALGTPLMGEYAGAVDRHYITLGAPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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; Sequence 59399, Application US/10450763
; Publication No. US2080196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR PILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR PILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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OTHER INFORMATION: Xaa = X or * as defined in Table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 9.6%; Score 225.5; DB 5 Local Similarity 35.7%; Pred. No. 6.9e-12; nes 65; Conservative 22; Mismatches 82
NUMBER OF SEQ ID NOS: 60736
SOFTWARR: Custom
SEQ ID NO 54683
LENGTH: 1118
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ORGANISM: Homo sapiens
                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: NAME/KEY: misc_feature
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LENGTH: 628
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APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr, Grant
Yamamoto, Robert
Forsyth, R.
                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-282-122A-56343
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Acvalic David K
APPLICANT: Acvalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

WINNER OF SEQ ID NOS: 2865684

SEQ ID NO 206691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 193992, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Sov. Yongwei
APPLICANT: Sov. Yongwei
APPLICANT: Sov. Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
LENGTH: 88
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                                                                                                                                                                      346
                                                                                                                                                                                                                                                  347 -GALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALN-----RLIMAQDTGSAIDG 400
                                                                                                                                                                                                                                                                              114 AKQFFERYFTPWQVAG-NGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 DKGYLK------LGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPV
                                                                                                                             Gaps
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                                                                                    Length 628;
                                                                                Query Match 5.9%; Score 138; DB 5; Length 628 Best Local Similarity 32.0%; Pred. No. 0.00075; Matches 48; Conservative 14; Mismatches 58; Indels
; LOCATION: (1)...(628)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-59399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_108501C.1.pep
US-10-425-115-193992
                                                                                                                                                                                                                                                                                                                                    401 AVRVDYFWGYGDEAGELAGKQKTTGYVWQL 430
                                                                                                                                                                                                                                                                                                                                                                  594 Q-HFDIYQGIGPEAGHRAGWYNHYGRVWVL 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 AGLRSGKALVRIRQTGKNSGTID 195
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US-10-425-115-193992
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US-10-424-599-206691
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Sec. 4.24

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AFPLICANT: AU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR PILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: G0/207,727
FRIOR APPLICATION NUMBER: G0/207,335
FRIOR PILING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: G0/230,335
FRIOR FILING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: G0/230,335
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-010-23
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
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FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-22
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                                                                                                                                                                                                                                                                                      133 LAGTVTGYYEPVLKGD-------DRRTAQARFPIYGIPDDFISVPLPAG---
                                                                                                                                                                                                       Indels 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 GPLSAGSGVFBAKISGK------GGHAAIPQLSIDPILAATIVI----
                                                                                                                        Query Match 4.7%; Score 111; DB 4; Length 440; Best Local Similarity 21.6%; Pred. No. 0.18; Matches 75; Conservative 47; Mismatches 96; Indels 1:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2866C.1.pep
US-10-424-599-206691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 56343, Application US/10282122A; Publication No. US20040029129A1
; GENERAL INFORMATION:
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US-10-484-218-22

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23;
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SCOFWARE: Patentin version 3.1
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4.6%; Score 108; DB 4; Length 676;
Best Local Similarity 21.6%; Pred. No. 0.63;
Matches 91; Conservative 40; Mismatches 112; Indels 178;
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; Publication No. US2005095633A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
    TITLE OF INVENTION: LACTIC ACID BACTERIA
    TITLE OF INVENTION: LACTIC ACID BACTERIA
    TITLE OF INVENTION: LACTIC ACID BACTERIA
    TITLE OF INVENTION: LACTIC ACID BACTERIA
    TITLE OF INVENTION: LACTIC ACID BACTERIA
    CURRENT FILING DATE: 2001-01-20
    CURRENT FILING DATE: 2004-01-20
    PRIOR APPLICATION NUMBER: EP 01202752.0
    PRIOR APPLICATION NUMBER: EP 01202841.1
    PRIOR APPLICATION NUMBER: EP 01202841.1
    PRIOR PILING DATE: 2001-07-20
    PRIOR PILING DATE: 2001-07-20
    PRIOR PILING DATE: 2001-07-25
    NUMBER OF SEQ ID NOS: 30
    SOFTWARE: PATENTIN VET: 3.2
    SEQ ID NO 22
    IBNOT DATE: 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-56343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEW----DEH-
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10(52052)8
FILE REPRENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                             470 MSTDGSAYHSNAALDSQVIFESFS----NFQAMPTSHDTYTNVVLANHADQLHDWGITSV 525
                                                                                                                                                                                                                                                                                     526 QLAPQYRSSTDGTFLDAIIQNGYAFTDRYDLGFGTPTKYGDDTDLRNVIKALHANGMQVM 585
                                                                                                                                                                                                                                                                                                                             ---IPDDFISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIK 218
                                                                                                                                                                                                                                                                                                                                                  KTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQ 327
                                                                                                                                                                                                                                             -----NGSLAGTV-------TGYYEPVLKGDDRRTAQARFPIYG----- 161
                                                                                                                                                                                                                                                                                                                                                                                                        GRFE---GSRFL-----PYHTRNQINGGALDGKAPILGYAEDPVELFFMHIQGSGRL 267
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                                                                                 35 SVINGPDRPVGIPDPAGTTVGGGGAVYTVV-PHLS--LPHW-----AAQDFAKSLQSFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 KALNRLIMAQDIGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVWQLLPNGM 435
                                          Indels 172;
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    Length 1006;
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                                          49; Mismatches 150;
    4.5%; Score 106; DB 5; 21.6%; Pred. No. 1.7;
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Publication No. US20030233675A1
GENERAL INFORMATION:
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US-10-369-493-17897
Query Match
Best Local Similarity
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Best Local Similarity
Matches 80; Conserv
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                                       Matches 102;
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APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICATION Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT PILING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
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PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-12-21
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                                             229 YHTRNQINGGALDGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYV 288
                                                                                                                                  289 --SIGRYMADKGY-----LKLGQTSMQGIKSYMRONPORLAEVLGQNPSYIFF--- 334
                                                                                                                                                                                245 GCAMGEYFRDNGMHAVIVYDDLSKQAVAYRQMSLLLRRPPGREA-----YPGDVFYLHSR 299
                                                                                                                                                                                                                             335 -RELAGSSND----GPVGALGTPLMGEYAGAVDRHYIT-----LGAPLFVAT--AHPVTR 382
                                                                                                                                                                                                                                                                                                                     383 KALNRLIMAQDIGSA-----IDGAVRVDY-----FWGYGDEAGELAGKOKITGY 426
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                                                                            210 QIVRQLEENGAMEYSIVVAATASEPAPLQFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-282-122A-52178
; Sequence 52178 Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITAA.034

CURRENT APPLICANTON NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

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                                                                                                                                                                                237 GGALDGKAPILGYAEDPVELF----FMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIG- 291
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224 ECPDTDMIIRSLEYCANRNGIELTAEEKGGLVVIKSFGLSAHGSTPEIGKNAIMQMFKFL 283
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                      90;
   4.4%; Score 102; DB 4; Length 463; 22.0%; Pred. No. 1.4; ive 51; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 FVATAHPVTRKALNRLIMAQDTGSAIDG-AVRVDYF 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 55128, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                      Conservative
                               Similarity
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Query Match
Best Local Simi
Matches 74;
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TVTGYYEPVLKGDDR-----RTAQARFPI----YGIPDDFIS-----VPLP--- 172
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                                                                                                                                                                                                                                                                                                                                       Query Match 4.4%; Score 102; DB 4; Length 627;
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Matches 69; Conservative 39; Mismatches 114; Indels 90; Gaps
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319 ADAYLEIAHTPN 330
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Sequence 10054, A
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Sequence 21474, A
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15614, A
22, Appli
262, App
24665, A
3465, A
30850, A
32439, A
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15978, A
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                                                                                                  ; Search time 26 Seconds (without alignments) 1402.307 Million cell updates/sec
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Sequence 6,
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US-09-072-279-14
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
               GenCore (c) 1993
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seq length: 200000000
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Sequence 6, Appli
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Sequence 20870, App
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14, Appl
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ALIGNMENTS
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PRUCINAL WOORWATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 LAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQTGKNSG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.9%; Score 605.5; DB 2; 33.7%; Pred. No. 1e-54; ative 60; Mismatches 154;
US-09-252-991A-19425
; Sequence 19425, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Matches 143; Conservative
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12;

Gaps

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 TGKNSGTIDNT------GGTHTADLSRPPITARTTAIKGRFEGSRFLPYHT-- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 INQTSSRLYNSNQDTYQAVENWLRSGADTRQLRQFNIAAFQMEGEDNYGNVKFTGYYTPV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TRKALNRLIMAQDIGSAIDGAVRVDYFWGYGDEAGELAGKQKTIGYVWQL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 LDNTGKFTGQYQMRLMVALDVGGAIKGH-HFDIYHGIKEAGQMAGFYNHYGRVWVL 353
                                                                                                                                                                                                                                                                                                                                                      131 GSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLP----AGLRSGKALVRIRQ
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larity 21.0%; Pred. No. 0.012;
Conservative 36; Mismatches 146; Indels 1.
                                                                                                                                                                                                                                                                   Length 365;
                                                                                                                                                                                                                                                                   Query Match 11.8%; Score 275; DB 2; Length 36 Best Local Similarity 27.5%; Pred. No. 4.5e-20; Matches 98; Conservative 47; Mismatches 140; Indels
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 TTVGGGGAVYT----VVPHLSLPHWAAQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GIAAAILAACQSKSIQTFPQPDTSVINGPDRPVG
                 FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6366
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. Patent No. 6551795
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                                                                                                                                                                                                        ; ORGANISM: Proteus mirabilis US-09-543-681A-6366
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Best Local Similarity
Matches 87; Conserv
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; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
                                                                                                                                                                                                                Sequence 10054, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
FILLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10054
                         95 DTRTLRQFGIDAWQMQGVDNYGNVQFTGYXTPVVQARHTRQGEFQYPIYRMPP----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNOINGGALDGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIR-IGYADKNEHPYVSI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRYMADKGYLKLGQTSMQGIKSYMRQNPQ-RLAEVLGQNPSYIFFRELAGSSNDGPV-GA 348
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    430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FTPWQVAGNGSLAGT-VTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 PAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GIAAAILAACQSK-----SIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAVYTV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----DFSEQVNQIRNASPRLYNSQS------NVYNALQEWLRAGG 94
  371 PLFVATAHPVTRKALNRLIMAQDTGSAIDGAVRVDYFWGYGDEAGELAGKQKTTGYVWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GAMLAMLAACSSKPTDRGQQYSDGKFTQP-FSLVNQPD-AVGAPINAG-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 314.5; DB 2; Length 3 26.6%; Pred. No. 3.2e-24; iive 47; Mismatches 148; Indels
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ORGANISM: Klebsiella pneumoniae
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                                                                                431 LPNG 434
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US-09-489-039A-10054
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US-09-543-681A-6366
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LENGTH: 1190
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244 AAGAGAGHARCAAGAVARRSAGHLAGRPARLALGLRPVVADRAAAGRLGAA---QRAG 300
                                                     -----GNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISV-----PLPAG 174
                                                                                                                                                                 358 GPAGIRQRRGGNLAGRRAGRPAPAADGPGQPGAVRRGGAGAVPGRSLELAGVRRPGPLG 417
                                                                                                                                                                                                    L----RSGKALVRI----RQTGKNSGTIDNTGGTHTA-------DLSRFP 209
                                                                                                                                                                                                                           210 ITARTTAIKGRFEG----SRF----LPYHTRNQINGGALDGKAPILGYAEDPVELFF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ACTYAFARAQFAACGGEGAQXQXDDDQLVVDSAELRPVAVPRPAQQREGGASGDPTPPKS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LSL---PHWA-----AQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ERYFTPWQVAGN-----INGSLAGTVTGYYEPVLKGDDRRTAQARFP----ING-- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 RSCLTAWMQKNNQCCPMDNKRLSARARHLSGQ----LHAPRDRATQARLPQLLAGLFGGC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 -----IPDDFISVPLPAGLRSGKALV---RIRQTGKNSGTIDNTGG-----THTAD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 LAHRTASPSAQLSLSAAAGAAGGEVPVCQDQVRFCGPTRD--QSVGGAPQGRHAASHAAD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTIONS: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PELLING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                 478 ATADRL---GRRAGLGQCRARFPRRPARLÞQGIVRAPESGAIDGAAÞ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AALYGIAAAILAACQSKSIQTFPQPDTSVINGPD-RPVGIPDPAGTTVGGGGAVYTVVPH
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                                                                                                                                                                                                                                                                                                                                                                             ----GKGKKAAGLRTFIHLGYLDRSVSNIHRVEIPAVTWRSSAMQRNPLSLRRTS 572
                                                                                                                                                                                                                                                                                                                                                      259 MHIQGSGRLKTPSGKYIRIGYADKN-----EHPYVSIGRYMADKGYLKLGQTS 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.7%; Score 110.5; DB 2; Length Best Local Similarity 23.9%; Pred. No. 0.0076; Matches 60; Conservative 25; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-252-991A-21474
'Sequence 21474, Application US/09252991A
'Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-270-767-45316
Sequence 45316, Application US/09270767
Petent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45316
LENGTH: 342
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US-09-270-767-45316
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八色学 少星精生生素化工人

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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107136, 136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
RIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 PYPDQA---NPSAEYWNPRNDPATWQHMVTYTLGLG----LTTSLTSPKWEGSTYSGGY 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 IYGIPDDFISVPLPAGLRSGKALVRIRQTGK-NSGTIDNTGGTHTAD----LSRFPITAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 KSLQSFRLGCANLKNRQG-----WQ------DVCAQAFQTPVHSFQAKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 DEIAAGRISWPNASNNHSNNVYDLWHAAVNSRGEFFSADSPDOLVAAFQDILNRISGKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------PSGNYSTFAEAQKTRAPRVYVG---ANDGML 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.4%; Score 102.5; DB 2; Best Local Similarity 22.2%; Pred. No. 0.35; Matches 76; Conservative 33; Mismatches 126;
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APPLICANT: Volchegursky, Yanina
TITLE OF INVENTION: Recombinant Megalomicin Bio
TITLE OF INVENTION: Genes and Uses Thereof
FILE REPERENCE: 300622004700
CURRENT APPLICATION NUMBER: US/09/679,279
CURRENT APPLICATION NUMBER: US 60/158,305
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 2000-03-17
NUMBER OF EQ ID NOS: 34
SOFTWARE: FRSESE FOR WINGOWS VERSION 4.0
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Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
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APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                            | | | :: ::: | | | | | | : ::| | GRSTNDFSIGIEH-GGYASSASFSTGMITTSAKLICNITRDQGIPRDSYHIVAHGRLQPE 376
133 LAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQTGKNSG 192
                                                                                                                                                                                              ---KFA 215
                                                                                                                                                                                                                                                                                                                                      :| | : : : | : : SGCWSWLINSAAGVSAHYVVNESGTEVSQLVRESSRAWHVAAAY---RSSLNGGVKSNLN 317
                                                                                                                  ----S 171
                                                                                                                                                         DP-VELFFWH-----IQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYLKLG 303
                                                                                                                                                                                                                                     304 QTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLM-----GEY 357
                                                                                                                                                                                                                                                                                                                 --LGAPLFVATAHPVTRKALNRLIMAQDT 394
                                                                                                                                                                                                                                                                                                                                                                                             G-SAIDGAVRVDYFWGYGDEAGELAGKOKTTGYV-------WQLLPNG-MKPE 438
                                                                             TIDNTGGTHTADLSRF-PITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPILGYAE 251
                                                                                                  97 FEGRPAAFGLLALRGQLITDGAA---LAGVSADAVRDEPLANLRAGAALL
                                                                                                                                                                                          DPDIQAHYIHNDVYSVLREGAGAF-TPAGK-VAVSLESTQVNP---
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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US-08-311-731A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08311731A; Patent No. 6583266; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   358 AG-----AVDRHYIT----
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ATGRNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 anino acids
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STREET: 600.
CITY: BOSTON
STATE: MASSACHUSETTS
TATE: MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||::| | || ||::| | || || || AAVWG----VLRCAQAES-----PDRFVLVDGDPETPPAVPDNPQLAVRDGAVFVPRLT 2801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ESARLLADGGVFVEMGKTDLRPAE 3057
                                                                                                                                                                                                                                                                                                                                                                                                                                      227 LPYHTRNQINGGALDGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 YVSIGRY----MADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSN 342
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                                                                                                                                                                                                --LGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFERYFTPWQVAGNGSLAGTVTGYYEP 143
                                                                                                                                                                                                                                                                            VLKGDDRRTAQARFPIYGIPD----DFISVPLP-----AGLRSGKALV---RI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 DGPVGALGTPLMGEYAGAVDRHYITL----GAPLFVATAHPVTRKALNRLIMAQDTGSAI 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Stater, Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

APPLICANTON: WAxcoccus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849) B.

CURRENT APPLICATION NUMBER: 08/09/902,540

CURRENT FILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                      185 RQTGKNSGTIDNTGGTH---TADLSRFP-----ITARTTAIKGRF---EGSRF
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    Gaps
                                                                                                                    -----GGGGAVYTV----VPHLSLPHWAAQDFAKSLQ---SFR--
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19.5%; Pred. No. 0.28;
tive 59; Mismatches 158; Indels 171;
57; Mismatches 155; Indels 192;
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                                      8 AALYGIAAAILAACQSKSIQTFPQPDTSVI--NGPDRPVGIPDPAGTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15614, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3020 VDV-VLNSLTGDLLD-----
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104; Conservative
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ORGANISM:
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; ORGANISM: Mycobacterium tuberculosis US-09-712-363-262
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                                                                                          84 FRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFERYFTPWQVAGNGSLAGTVTGYYEP 143
                                                                                                                                         181
                                                                                                                                                                                     182 VRIRQTGKNSGTIDNTGGTHTADLSRFP-ITARTTAIKGRFE--GSRFLPYHTRNQINGG 238
                                                                                                                                                                                                            475 IEEL------VLAAPLVMHPGVGVQVQVVVGAADESGHRAVSVYSRGDQSQG 520
                                                                                                                                                                                                                                   239 ALDGKAPILGY--AEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMAD 296
                                                                                                                                                                                                                                                          521 WLLNAEGMLGVAAAETPMDLSVWPPEGAESVD-----ISDGYAQ-----LAE 562
                                                                                                                                                                                                                                                                                 KGYLKLGQTSMQGIKSYMRQNPQRLAEV-----LGQNPSYI-----FF 334
                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DDFISVPLPAGLRSGKAL
                                                                                                                                                        27 QTFPQPDTSVIN--GPDRPVGIPDPAGTTVGGGGAVYTV-VPHLSLPHWAAQDFAKSLQS
                                                                                                                                                                                                                                                                                                                               RELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFV----ATAHPV--TRKALNR
                                                                                                                                                                                                                                                                                                                                                     621 KTOASTETRLPFCWRGVSLHAGGAGRVRARFASAGADAISVDVCDATGLPVLTVRSLVTR
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                                                                                                                                                                                                                                                                                                                                                                                                    681 PITAEQLRAAVTAA-----GGASDQGPLE-----VVWSPISVVSGGANGSAP 722
                         Gaps
Query Match
4.2%; Score 98.5; DB 2; Length 986;
Best Local Similarity 21.2%; Pred. No. 0.7;
Matches 101; Conservative 55; Mismatches 173; Indels 147;
                                                                                                                                       144 VLKG-----DDRRTAQARFPIYGIP--
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Patent No. 6892139
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APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
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TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPREBUCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-0-2-18 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NOS: 33142
                                                     25;
                                                                                                                                                                                                                                                                                                                         RELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFV----ATAHPV--TRKALNR 387
                                                                                                                                84 FRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFERYFTPWQVAGNGSLAGTVTGYYEP 143
                                                                                                                                                                                                                                           ------GGRRV----QLPTYAFQRRRFWE---TP-GADGPADAAGLGLGATEH 445
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                                                     Gaps
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  4.2%; Score 98.5; DB 2; Length 1616;
21.2%; Pred. No. 1.5;
tive 55; Mismatches 173; Indels 147;
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Query Match
Best Local Similarity 21.2*
Matches 101; Conservative
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----PAGT--TVGGGGAVYTV----VPHLSLPHWAAQ---DFAKSLQSFR-----LGCA 89
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
                                                                                                                            2875 POKADMGTEAAGVVTAVGPDVDAF----
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REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 495
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 3567 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
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CITY: Abbott Park
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                                    219 GRFEGSRFLPY--HTRNQINGGALDGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIR 276
                                                              283 SQGMDQQVGHPAQQVGDRAGLRIETLLAGEGKHPLGQVGAALGGLQGVLQEVGGALVAGQ 342
                                                                                                                                                                                                           343 AFLQQPEAADDHRQQVVEVVGHAAGEVPQGLHLLGLEGLLAGPFQFAFGFDPVGDV-TGY 401
                                                                                                                                                                                                                                                                                                 .----FLLETPF 440
181 QPGATPNSLGGVEGFHRTAQGFLVHAAAGVADAQADIVARCEAMGIVRRHPLVAR---- 235
                                                                                                            277 I-GYADKNEHPYVSIG------RYMADKGYLKLGQT-----SMQGI------K 311
                                                                                                                                                                                    SYMRQ-----NPQRLAEVLGQNPSYI-----FFRELAG----SSNDGPVGALGTPL 353
                                                                                                                                                                                                                                                              MGE-----YAGAVDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIDGAVRVDY 406
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ilarity 21.9%; Pred. No. 5.7;
Conservative 50; Mismatches 144; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Method for Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
TLING DATE: 17-JAN-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
                                                                                                                                                                                                                                                                                               402 LGEADQPAIAVADRIDHH---VGPEATAVLAHPPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J
TITLE OF INVENTION: Recombinant DNA Methor TITLE OF INVENTION: Erythromycin Analogs NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4952.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/07642734C Patent No. 5824513
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 495;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
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STATE: IL
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Best Local Similarity
Matches 106; Conserva
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2815 SALTLPAGTQRLVPGDGAIDSVAFEPAPDVEQPLRAGEVRVDVRATGVNFRDVLLALGMY 2874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3064 ----AGDFRGRYAPFDLGEA----- 3091
                                              NLKNRQGWQDV-CAQAFQTPVHSFQAKOFFERYFTPWQVAGNGSLAGTVTGYYEPVLKGD 148
                                                                                                                                                                                                                                                                                                                               225 RFLPYHTRNQINGGALDGKAPILGYAEDPVELFFWHIQGSGRLKTPSGKYIRIGYADKNE 284
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Sequence 36439, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
FRICK FILING DATE: 1998-02-18
FRICK FILING DATE: 1998-02-18
FRICK FILING DATE: 1998-02-18
FRICK FILING DATE: 1998-02-18
FRICK FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                   311 VLENVMLAPRKVLGKSRABABADKÖLTHVGLGDKLKVFPORLSGGOOORMAIARALAM 370
                                                                                                                                                                                                                                                                       NPSYIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNR 387
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                                                            -RPAGTEMAAMIEISGVHKA-YGQFEV-----VKGVDLRVDKGEVL----SIIGGSG 254
                                                                                                                                                                                     I------AEVLGQTSMQGIKSYMRQNPQRL-----AEVLGQ
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                       --RFEGSRFLPYHTRNQINGGAL
                                                                                                       DGKAPILGYAE--DPVELFFMHIQG-----SGRLKTPSGKYIRIGYADKNEHPYVS
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                       IROTGKNSGTIDNTGGTHTADLSRFPITARTTAIKG-
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US-09-252-991A-32439
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                                                                                                                                                                                   2759 AAMWG----VIRCAQAESPDRFVILDTDAEPGMLPAVPDNPQLALRGDDVFVPRLSPLAP
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                                                                                                                                              -VGIPD----
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al Similarity 21.9%; Pred. No. 5.7;
106; Conservative 50; Mismatches 144; Indels 184;
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                                                                                                                                            8 AALYGIAAAILAACQSKSIQTFPQPDTSVING-----PDRP-----
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30850
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US-09-252-991A-30650
; Sequence 30850, Application US/09252991A
; Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
Matches 69; Conserva
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MOLECULE TYPE:
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US-08-439-009A-4
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321 LAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFVATAHPV 380
                                          456 LESVLWOHPS-IF-----DAGVAGVPDPVAGELPGAV------VVLESGKNM 495
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15978
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4.1%; Score 95.5; DB 2; Length 1803;
Best Local Similarity 18.4%; Pred. No. 3.6;
Matches 102; Conservative 68; Mismatches 172; Indels 211; Gaps
                                                                                                                    ---LDGKAPILGYAEDP-VELFFMHIQGSGRL---
                                                                                        TRKALNRLIMAQ-DTGSAIDGAVRVDYFWGYGDEAGE-LAGK
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                                                                                                                                                                                                                                           ; Sequence 15978, Application US/09902540; Patent No. 6833447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 YVWQ----LLPNG 434
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 DRRTAQA-----
                                                                                                                                                                                                    RESULT 17
US-09-902-540-15978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 LTVVPFHHGFGMFTTLGYLICGFRVVMLTKFDEETFLKTLQDYKCTSVILVPTLFALLNK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 ANLKONRQGWQDVCAQAF-QTPVHSFQAKQFFERYFTPWQVAGNGSLAGTVTGYYEPVLKG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPITARTTAIKGRFEGSRFLPYHTRNQINGGALDGKAPIL--GYAEDPVELFFWHIQGSG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 RLKTPSGKYIRIGYADKNEHPYV----SIGRYMADKGYLKLGQTSMQGIKSYMRQNPQR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 SELLNKYDLSNLVEIÅSGGAPLSKEVGEALARRFNLPGVRQGYGLTETTSAIIITP--EG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 DDRRTAQARFPIYGIPDDFISVPLPAGLRSGKALVRIRQTGKNSGTIDNTGGTHTADLSR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DPA-GTTVGGGGAV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
4.1%; Score 95.5; DB 2; Length 548;
Best Local Similarity 20.8%; Pred. No. 0.59;
Matches 96; Conservative 47; Mismatches 148; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 DDKPGASGKV------VPL-----FKAKVIDLDTKKSLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,183A FILING DATE: US-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ACQSKSIQTFPQPDTSVINGPDRPVGIP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/467,773
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,081
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Scanlon, William J.
REGISTRATION NUMBER: 31,136
REFERENCE/DOCKET NUMBER: 19017/166
TELECOMMUNICATION INFORMATION:
                                                                                 APPLICANT: WOOD, Keith V.
APPLICANT: GRUBER, MONIKA G.
TILLE OF INVENTION: MUTANT LUCIFERASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & Lardher
STREET: P.O. BOX 1497
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER! IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                Sequence 12, Application US/08487183A Patent No. 6387675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (608)258-5035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                Madison
                                                                                                                                                                                                                                                                                             USA
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US-08-487-183A-12
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CITY: Ma
STATE: W
                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 VRQGY-----GLIETTSAIIITPEGDDKPGASGKVVPLFKAKVIDLD----TKKTLGP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 KGRFEGSRFLPYHTRNQINGGALDGKAPIL--GYAEDPVELFFMHIQGSGRLKTPSGKYI 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 -IGYYDEEKHFFIVDRLKSLIKY---KGY------QVPPAELESVLLQHPN 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 KSIQTFPQPDTSVINGPDRPVGIP-------DPA-GTTVGGGGAVYTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 PFHHGFGMFTTLGYLTCGFRIVMLTKFDEETFLKTLODYK-----
                                                                                                                                                                                                                                                                                                        SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,047
FILING DATE: 19920623
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
FEGITATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 AQ-DTGSAIDGAVRVDYFWGYGDE-----AGELAGK 420
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19.7%; Pred. No. 0.75;
7ative 56; Mismatches 147;
         Luciferase Of Firefly
                                                                                                1155 Avenue of the Americas
                                                                                                                    CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CONTUTER: IBM PC COMPATING
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                               Pennie & Edmonds
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
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66141 PENNIE
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                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
         OF INVENTION:
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Best Local
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                                                                                                                                                                                                          APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23628
LENGTH: 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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Thermostable Luciferase Gene Of Firefly, No. 5229285e
DNA, And Process For The Preparation Of Thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YTVVPHLSLPHWAAQDFAKSLQS-----FRLGCANLKNRQGWQDVCAQAFQTPVHSF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 QAKQFFERYFTPWQVAGNG----SLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFIS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 VPLPAGLRSGKALVRIRQ---TGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PVGQLAG-ALARVQPLPLPGSELGVV-----749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 FLPYHTRNQINGGALDGKAPILGYAEDPVELFFMHI------QGSGRLKTPSGKYI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 RIGYADKNEHPYVSIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELAGSSNDGPVGALGTPLMGEYAGAVDRHYITL -----GAPLFVATAHPVTRKAL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 833 ---GEVDELP-----GELAPLVD----TLOGRAVALEETRAQRFVAFDQPLEAGAQ 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 ------PQAVARGGRRLARRARMVGGQFQ-----HRRRVAQA-FP----- 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750 -----rRQV-----GRLAAAGFGVEPREFVEQQVQRPTIGDDVMQGDPELVL---LFV 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 RAALYGIAA-AILAACQSKSIQTFPQP-----DTSVINGPDRPVGIPDPAGTTVGGGGAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.1%; Score 95; DB 2; Length 1411;
21.8%; Pred. No. 2.8;
ive 42; Mismatches 127; Indels 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23628, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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877 RRFVQLAAQAQAAGDVVGGALRID 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 NRLI----MAQDTGSAIDGAVRVD 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/07903047
Patent No. 5229285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kajiyama, Naoki
APPLICANT: Nakano, Eiichi
TITLE OF INVENTION: Thermost.
TITLE OF INVENTION: Thermost.
TITLE OF INVENTION: DNA, And
||:| | |:|
925 YVYQEGMILSPDG 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 97; Conserv
                                                                                                                      -09-252-991A-23628
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US-07-903-047-8
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BIOTINYLATED FIREFLY LUCIFERASE, A GENE
FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
ANALYSIS METHOD
                                338 VRQGY-----GLTETTSAIIITPEGDDKPGASGKVVPLFKAKVIDLD----TKKTLGP 386
                                                                                                                              276 RIGYADKWEHPYV----SIGRYMADKGYLKLGQTSMQGIKSYMRONPORLAEVLGQNPS 330
                                                                                                                                                                                                                                                                                                          331 YIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNRLIM 390
162 IPDDFISVPLPAGLRSGKALVRIRQTGKN----SGTIDNTGGTHTADLSRFPITARTTAI 217
                                                                                                218 KGRFEGSRFLPYHTRNQINGGALDGKAPIL--GYAEDPVELFFMHIQGSGRLKTPSGKYI 275
                                                                                                                                                                                                                                                       -----QVPPAELESVLLQHPN 465
                                                                                                                                                                                                                                                                                                                                                           -----VVLEKGKSMTEKEVMDYVA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KIKUCHI, MAMORU
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINVLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BI
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BI
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                391 AQ-DIGSAIDGAVRVDYFWGYGDE----AGELAGK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                              466 -IF-----DAGVAGVPDPIAGELPGAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13.JAN-1997
CLASSIFICATION: 435
FRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: UP 193798/1994
FILING DATE: 27-JUL-1994
FILING DATE: 27-JUL-1994
FILING DATE: 27-JUL-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 24-APR-1995
FILING DATE: 24-APR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
                                                                                                                                                                                                                                       ||| |::| :: | || || || 425 -IGYYDEEKHFFIVDRLKSLIKY---KGY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08782118
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FUKUDA, SATOSHI APPLICANT: KIKUCHI, MAMORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acid
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FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
ANALYSIS METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 KTVEVNRKEQVALÍMNSSGSTGLÞKGVQLTHENLVTRFSHARDÞÍYGNQVSPGTAILÍTVV 243
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19.7%; Pred. No. 0.75;
tive 56; Mismatches 147; Indels 163;
                                                                                                                                                                                                                                                                                                                                                        OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
                                                                                                                                                                                                                                                                                                                                                                                                              : 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 193798/1994
FILING DATE: 27-UUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 54625/1995
FILING DATE: 14-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 98857/1995
FILING DATE: 24-APR-1995
ATTONNEY, AGENT INFORMATION:
NAME: 08LON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMBUTER: IBM PC compatible
AVETEM: PC-DOS/MS-DOS
AVETEM: PC-DOS/MS-DOS
                  Sequence 2, Application US/08460934 Patent No. 5814465
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                                                                GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
TITLE OF INVENTION: FOR BIOTIVITIE OF INVENTION: FOR BIOTIVITIE OF INVENTION: PROCESS FITTLE OF INVENTION: PROCESS FITTLE OF INVENTION: ANALYSIS NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 90; Conserva
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US-08-460-934-2
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MEDIUM TYPE: Floppy disk
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US-09-111-752-14
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APPLICANT: KAJIZAWA, NAOKI
APPLICANT: KAJIZAWA, NAOKI
APPLICANT: KAJIZAWA, NAOKI
APPLICANT: MURAKAMI, SELJI
TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND
TITLE OF INVENTION: PROCESS POR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN
NUMBER OP SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                             184 KTVEVNRKEQVALIMNSSGSTGLPKGVQLTHENLVTRFSHARDPIYGNQVSPGTAILTVV 243
                                                                                                                                                                                                                                                                                                                     PH------LSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAF 105
                                                                                                                                                                                                                                                                                                                                             244 PFHHGFGMFTTLGYLTCGFRIVMLTKFDEETFLKTLQDYK--------CSSVI 288
                                                                                                                                                                                                                                                                                                                                                                                                                          289 LVPTLPAILNRSELLDKYDLSNLVEIASGGA-----PLSKEIGEAVAR-RFNLPG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 IPDDFISVPLPAGLRSGKALVRIRQTGKN----SGTIDNTGGTHTADLSRFPITARTTAI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : | | : : | | : : | 338 VRQGY-----GLTETTSAIIITPEGDDKPGASGKVVPLFKAKVIDLD----TKKTLGP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 KGRFEGSRFLPYHTRNQINGGALDGKAPIL--GYAEDPVELFFWHIQGSGRLKTPSGKYI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 NRR------GEVCVKGPMLMKGYVDNP-EATREIIDEEGWLHTGD---- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 RIGYADKNEHPYV----SIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQNPS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 -IGYYDEEKHFFIVDRLKSLIKY---KGY--------QVPPAELESVLLQHPN 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 YIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNRLIM 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - IF-----DAGVAGVPDPIAGELPGAV------VVLEKGKSMTEKEVMDYVA 505
                                                                                                                                                                                                                                                                                                                                                                                                 106 QTPV--HSFQAKQFFERY--FTPWQVAGNGSLACTVTGYYEPVLKGDDRRTAQARFPIYG 161
                                                                                                                                                                                                                                        24 KSIQTFPQPDTSVINGPDRPVGIP-------DPA-GTTVGGGGAVYTVV 64
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                56; Mismatches 147; Indels 163;
                                                                                                                                                           Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
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                                                                                                                                                             DB 1;
                                                                                                                                                                              0.75;
                                                                                                                                                         Query Match

4.0%; Score 94.5;
Best Local Similarity 19.7%; Pred. No. 0.
Matches 90; Conservative 56; Mismatche
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APPLICATION NUMBER: US/09/111,752
FILING DATE: 08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09111752
Patent No. 6074859
GENERAL INFORMATION:
                                                     MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Luciola lateralis
                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-JUL
CLASSIFICATION: 435
                                       unknown
TYPE: amino acid
STRANDEDNESS: sir
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                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-111-752-14
                                                                                                   US-08-782-118-2
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65 PH-----LSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAF 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : | | : | | : | | 338 VRQGY-----GLTETTSAIIITPEGDDKPGASGKVVPLFKAKVIDLD----TKKTLGP 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 LVPTLFAILNRSELLDKYDLSNLVEIÅSGGA------PLSKEIGEAVAR-RFNLPG
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LOWE, CHRISTOPHER ROBIN
MURRAY, JAMES AUGUSTUS HENRY
TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
4.0%; Score 94.5; DB 2; Length 548;
Best Local Similarity 19.7%; Pred. No. 0.75;
Matches 90; Conservative 56; Mismatches 147; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 AQ-DTGSAIDGAVRVDYFWGYGDE----AGELAGK 420
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                                                                                             7126-0009-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 KSIQTFPQPDTSVINGPDRPVGIP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SQUIRRELL, DAVID JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09380061B; Patent No. 6265177; GENERAL INFORMATION:
                          NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126:
TELECOMMULICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: amino acid
STRANDEDNESS: single
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DPA-GTTVGGGGAVYTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 94.5; DB 2; Length 548;
19.7%; Pred. No. 0.75;
tive 56; Mismatches 147; Indels 163;
                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHLIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,061B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 PFHHGFGMFTTLGYLTCGFRIVMLTKFDBETFLKTLQDYK-----
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                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-APR-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-APR-1997
ATTONEY/AGNT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 124-725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-380-061B-16
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Patent No. 6387675
GENERAL INFORMATION:
APPLICANT: WOOD, Keith V.
APPLICANT: GRUBER, Monika G.
TITLE OF INVENTION: MUTANT LUCIFERASES
COMPUTER: IBM PC compatible
                                                                                                          FILING DATE: 25-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 19.7'
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- DPA-GTTVGGGGAVYTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
4.0%; Score 94.5; DB 2; Length 548;
Best Local Similarity 19.7%; Pred. No. 0.75;
Matches 90; Conservative 56; Mismatches 147; Indels 163; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 PFHHGFGMFTTLGYLTCGFRIVMLTKFDEETFLKTLQDYK-----
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,183A FILING DATE: 06-JUN-1995 CLASSIFICATION NUMBER: US 08/467,773 PRIOR APPLICATION NUMBER: US 08/467,773 PRIOR APPLICATION NUMBER: US 08/177,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| :| || : || || SQVSNAKRLRGGVR-----FVDEVPKGLTGKIDGK 535
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COUNTRY: USA
ZIP: 53701-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 KSIQTFPQPDTSVINGPDRPVGIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Scanlon, William J.
REGISTRATION NUMBER: 31,136
REFERENCE/DOCKET NUMBER: 1901'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (608) 258-4258
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (608)258-5035

    Foley & La
P.O. Box 1497

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                          Madison
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184 KTVEVNRKEQVALIMNSSGSTGLPKGVQLTHENAVTRFSHARDPIYGNQVSPGTAILTVV 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 PPHHGFGMFTTLGYLTCGFRIVMLTKFDEETFLKTLQDYK-------CSSVI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 QTPV--HSFQAKQFFERY--FTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 LVPTLFAILNRSELLDKYDLSNLVEIÅSGGA------PLSKEIGEAVAR-RFNLPG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 4.0%; Score 94.5; DB 2; Length 548; Similarity 19.7%; Pred. No. 0.75; 00; Conservative 56; Mismatches 147; Indels 163;
                                                                                APPLICANT: Hold, Keith V.
APPLICANT: Hall, Mary P.
TITLE OF INVENTION: Thermostable luciferases and methods of TITLE OF INVENTION: Thermostable luciferases and methods of TITLE OF INVENTION: Production
FILE REFERENCE: 341.012US1
CURRENT APPLICATION NUMBER: US/09/396,154
CURRENT FILING DATE: 1999-09-15
EARLIER APPLICATION NUMBER: US 09/156,946
EARLIER PILING DATE: 1998-09-18
EARLIER PILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ 1D NOS: 93
SOFTWARE: FASTSEQ for Windows Version 3.0
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                     Sequence 28, Application US/09396154
Patent No. 6602677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Luciola lateralis
US-09-396-154-28
                                                                  GENERAL INFORMATION:
US-09-396-154-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 28
LENGTH: 548
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Best Local S
Matches 90
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Sequence 4, Application US/09581241A
Patent No. 6812012
GENERAL INFORMATION:
APPLICANT: HATTOIN, NORIAKI
APPLICANT: MURAKAM, SELJI
TITLE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP USING THE

US-09-581-241A-4

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Sequence 6, Application US/09581241A

Sequence 6, Application US/09581241A

Patent No. 6812012

GENERAL INFORMATION:
APPLICAMT: HATTORI, NORIARI
APPLICAMT: HATTORI, SELJI
ITILE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP USING THE TITLE OF INVENTION: SAME
FILE REFERENCE: 193582US-3524-7126-0 PCT
CURRENT APPLICATION NUMBER: US/09/581,241A
CURRENT APPLICATION NUMBER: US/09/581,241A
CURRENT APPLICATION NUMBER: 1997/361022
PRIOR FILING DATE: 1997-12-26
RIOR FILING DATE: 1997-12-26
RIOR FILING DATE: 1997-13-26
RIOR FILING DATE: 1997-13-58
SOFTWARE PATENTH VERSION 3.2
SEQ ID NO 6
LENGTH: 548
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19.7%; Pred. No. 0.75;
vative 56; Mismatches 147;
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FILLE OF INVENTION: SAME
CURRENT APPLICATION NUMBER: US/09/581,241A
CURRENT APPLICATION NUMBER: US/09/581,241A
CURRENT FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: JP97/361022
NUMBER: PALENT 1997-12-26
NUMBER: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 548
                                                                                                                                                                                                                                                                      ; ORGANISM: Luciola lateralis
US-09-581-241A-4
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ORGANISM: Luciola lateralis
US-09-581-241A-6
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Best Local
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BIOTINYLATED FIREFLY LUCIFERASE, A GENE
FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
ANALYSIS METHOD
                                                                                                                                                                                                             276 RIGYADKNEHPYV----SIGRYMADKGYLKLGQTSMQGIKSYMRQNPQRLAEVLGQNPS 330
                                                                                                                                                                                                                                                                                              331 YIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNRLIM 390
                                                                                   338 VROGY-----GLTETTSAIIITPEGDDKPGASGKVVPLFKAKVIDLD----TKKTLGP 386
                                                                                                                            218 KGRFEGSRFLPYHTRNOINGGALDGKAPIL--GYAEDPVELFFMHIQGSGRLKTPSGKYI 275
                                                                                                                                                                      424
                                                                                                                                                                                                                                                    425 -IGYYDEEKHFFIVDRLKSLIKY---KGY------QVPPAELESVLLQHPN 465
                                                                                                                                                                                                                                                                                                                                       466 -IP------DAGVAGVPDPIAGELPGAV-------VVLEKGKSMTEKEVMDYVA 505
--PLSKEIGEAVAR-RFNLPG 337
                                           IPDDFISVPLPAGLRSGKALVRIRQTGKN----SGTIDNTGGTHTADLSRFPITARI 217
                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   391 AQ-DTGSAIDGAVRVDYFWGYGDE----AGELAGK 420
                                                                                                                                                                                                                                                                                                                                                                                                                          SOVSNAKRLRGGVR-----FVDEVPKGLTGKIDGK 535
  289 LVPTLFAILNRSELLDKYDLSNLVEIASGGA----
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PELLING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 14-MAR-1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08460934; Patent No. 5814465; Patent No. 5814465; ABENERAL INFORMATION: APPLICANT: TATSUMI, HIROKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 71.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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KIKUCHI, MAMORU
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP USING THE
TITLE OF INVENTION: SAME
FILE REFERENCE: 193582US-3524-7126-0 PCT
CURRENT APPLICATION NUMBER: US/09/581,241A
CURRENT FILING DATE: 2000-66-26
PRIOR APPLICATION NUMBER: J997/361022
PRIOR FILING DATE: 1997-12-26
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KTVEVNTKKEQVALIMNSSGSTGLPKGVQLTHENIVTRFSHARDPIYGNQVSPGTAILTVV
                                                                                     -DPA-GTTVGGGGAVYTVV
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19.7%; Pred. No. 0.75;
iive 56; Mismatches 147; Indels 163;
                                             163;
  4.0%; Score 94.5; DB 2; Length 548;
19.7%; Pred. No. 0.75;
tive 56; Mismatches 147; Indels 16
                                                                                                                                                                                                244 PFHHGFGMFTTLGYLTCGFRIVMLTKFDEETFLKTLQDYK----
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                                                                                24 KSIQTFPQPDTSVINGPDRPVGIP------
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Patent No. 6812012
GENERAL INFORMATION:
APPLICANT: HATTORI, NORIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.2 SEQ ID NO 8 LENGTH: 548
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                                           Conservative
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Best Local Similarity
                   Best Local Similarity
Matches 90; Conserv
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Patent No. 5843746
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUM, HIROXI
APPLICANT: FUKUCHI, MAMORU
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KIKUCHI, MAMORU
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
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                                                                                                                                                                                                                  --LSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAF 105
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                                                                                                                                                                                                                                                                                                          309 LVPTLFAILNRSELLDKYDLSNLVEIASGGA------PLSKEIGEAVAR-RFNLPG 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                         331 YIFFRELAGSSNDGPVGALGTPLMGEYAGAVDRHYITLGAPLFVATAHPVTRKALNRLIM 390
                                                                                                                                                                                                                                                                                    106 QTPV--HSFQAKQFFERY--FTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYG 161
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                                                                                                                    Gaps
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                                                                                 4.0%; Score 94.5; DB 1; Length 568; 19.7%; Pred. No. 0.79;
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                                                                                                                                                24 KSIQTFPQPDTSVINGPDRPVGIP----
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APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAM-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                90; Conservative
                               MOLECULE TYPE: protein
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amino acid
                                                                                                 Similarity
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204 KTVEVNRKEQVALIMNSSGSTGLPKGVQLTHENLVTRFSHARDPIYGNQVSPGTAILTVV 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 1; Length 568;
0.79;
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19.7%; Pred. No. 0.79;
tive 56; Mismatches 147;
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                                                                                                                                               FILING DATE: 27-ULL-1994

PRIOR APPLICATION DATA:
APPLICATION UNDERR: JF 54625/1995

FILING DATE: 14-WAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 98857/1995

FILING DATE: 24-APR-1995

ATTOMNEY GENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7126-001-0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
THE DATE: 05-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 71.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 19.7%
Matches 90; Conservative
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TOPOLOGY: linea.
TECHLE TYPE: protein
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RESULT 2
US-09-303-862-12
US-09-303-862-12
Sequence 12, Application US/09303862
Patent No. 6034230
GENERAL INFORMATION:
APPLICANT: Hessel, Andrew J.
APPLICANT: Neu M.D., Nikolaus
APPLICANT: Penninger, Josef M.
TITLE OF INVENTION: Disease
TITLE OF INVENTION: Disease
TITLE OF INVENTION: Disease
FILE REPERENCE: A-536
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Sequence 12, Appl
Sequence 10, Appl
Sequence 62, Appl
Sequence 100, Appl
Sequence 100, Appl
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCOMB.seq:*

8: /cgn2_6/ptodata/1/ina/PCOMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-082-649B-51

US-09-082-649B-56

US-09-082-649B-56

US-09-082-649B-56

US-09-082-649B-56

US-09-325-193A-90

US-09-325-193A-90

US-09-325-193A-90

US-09-321A-42

US-09-337-619-10

US-09-337-619-10

US-09-984-365-42

US-09-984-365-42

US-09-557-188A-2
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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Sequence 12, Application US/09133774B

Patent No. 5952636

GENERAL INFORMATION:
APPLICANT: Bachmaier, Kurt
APPLICANT: New M.D., Nikolaus
APPLICANT: New M.D., Nikolaus
APPLICANT: Penninger, Josef M.
TITLE OF INVENTION: Disease
FILLE OF INVENTION: Disease
FILLE OF INVENTION: Disease
FILLE OF INVENTION NUMBER: US/09/133,774B
CURRENT FILLING DATE: 1990-08-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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US-09-965-101-58

US-10-697-055-42

US-10-651-013-14

US-09-917-222B-1

US-09-954-987B-83

US-09-674-126B-83

US-09-082-649B-13

US-09-965-101-12

US-09-965-101-13

US-09-965-101-13

US-09-965-101-39

US-09-965-101-39

US-09-965-101-39

US-09-965-101-39

US-09-960-774-70

US-09-131-170-64

US-09-137-619-70

US-09-137-619-70

US-09-137-619-70

US-09-954-987B-34

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US-09-954-987B-34
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    SEQ ID NO 12
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RESULT 6
US-09-286-098-105
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TITLE OF INVENTION: UNMETHYLATED CPG DINUCLECTIDE IN THE TREATMENT OF TITLE OF INVENTION: UNMETHYLATED CPG DINUCLECTIDE IN THE TREATMENT OF TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS

TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS

TORRENT APPLICATION NUMBER: US/09/030,701B

CURRENT FILING DATE: 1990-02-25

PRIOR FILING DATE: 1997-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 10, Application US/08738652B

Batent No. 6207646

GENERAL INFORMATION:

APPLICATUR: KILOSMATION:

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7004 HCL

CURRENT APPLICATION NUMBER: US/08/738,652B

CURRENT FILING DATE: 1996-10-30

EARLIER FILING DATE: 1996-07-15

EARLIER FILING DATE: 1996-02-07

NUMBER OF SEQ ID NOS: 55

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PRAESEQ for Windows Version 3.0
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/303,862
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: 09/133,774
EARLIER FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 12
LENGTH: 20
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US-08-738-652-10
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LENGTH: 20
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Sequence 105. Application US/09286098

Sequence 105. Application US/09286098

Patent No. 6218371

GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: Cytokines
STILE REPRENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286,098
CURRENT APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 105
INVENTION: 20
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US-09-286-099-100
Sequence 100, Application US/09286098
Sequence 100, Application US/09286098
Sequence 100, Application US/09286098
SEQUENCE INVENTION: Methods and Products for Stimulating the TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: USWARER: US/09/286,098
CURRENT FILING DATE: 1999-04-02
SEARLIER APPLICATION NUMBER: US 60/080,729
SEARLIER APPLICATION NUMBER: US 60/080,729
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Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                             ; FEATURE:
. OTHER INFORMATION: synthetic oligonucleotide
US-030-701-62
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 62
LENGTH: 20
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 100
LENGTH: 20
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-082-649B-56
; Sequence 56, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION
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ORGANISM: Artificial Sequence
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Matches 20; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
ATTORNEY FACENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION: NUMBER: 38,347
REGISTRATION: NUMBER: 38,347
REGISTRATION: NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08960774

Patent No. 623916

GENERAL INFORMATION:

APPLICANT: Krieg et al.,

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA.
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1 Similarity 100.0%; Pred. No. 1;
20; Conservative 0; Mismatches 0; Indels
                                                                                                    Length 20;
                                                                                                                                         0; Indels
                                                                                                  DB 3;
                                                                                              Query Match
100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches
                                    ; OTHER INFORMATION: Synthetic Sequence US-09-286-098-105
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US-09-082-649B-51
; Sequence 51, Application US/09082649B
; Patent No. 6339068
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619/618-2099
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STRANDEDNESS: sing
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Matches 20; Conserv
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APPLICANT: Krieg, Arthur M.

APPLICANT: Schorr, Joachim
APPLICANT: W. Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REPERENCE: C1039/7009
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT FILING DATE: 1998-05-20
FRIOR APPLICATION NUMBER: US 60/047,233
FRIOR PILING DATE: 1997-05-20
FRIOR APPLICATION NUMBER: US 60/047,209
FRIOR PILING DATE: 1997-05-20
FRIOR PILING DATE: 1997-05-20
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APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
ITILE OF INVENTION: Vectors and Methods for Immunization or
ITILE OF INVENTION: Therapeutic Protocols
ITILE OF INVENTION: Therapeutic Protocols
ITILE OF INVENTION: Therapeutic Protocols
ITILE OF INVENTION: Therapeutic Protocols
ITILE OF INVENTION: Therapeutic Protocols
ITILE OF INVENTION: Therapeutic Protocols
ITILE OF INVENTION NUMBER: US 60/047,233
PRIOR PILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE PRACES FREE FRACES FOR WINDOWS VERSION 3.0
IEBNGTH: 20
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Pred. No. 1;
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     backbone
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NAME/KEY: misc_feature;
LOCATION: (0)...(0)
1.OTHER INFORMATION: Has phosphodiester backbuck-09-082-6498-56
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GENERAL INFORMATION: APPLICANT: Davis, Heather L.

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20; Conservative
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US-09-191-170-97
Matches
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US-09-325-193A-86

Sequence 86, Application US/09325193A

Patent No. 6406705

Patent No. 6406705

APPLICANT: Bavis, Heather I.

APPLICANT: Schorr, Joachim

APPLICANT: Krieg, Arthur M.

TITLE OF INVENTION: Unmerhylated CpG Dinucleotide as an Adjuvant

TITLE OF INVENTION: Unmerhylated CpG Dinucleotide as an Adjuvant

PILE REFERENCE: C1039/7025/HCL

CURRENT FILING DATE: 1999-06-03

PRIOR PILING DATE: 1998-06-16

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 86

LENGTH: 20

LENGTH: 20

LENGTH: 20

LENGTH: 20

LENGTH: 20

LENGTH: 20

LENGTH: 20
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OTHER INFORMATION: synthetic oligonucleotide
NAME/KST: misc. feature
LOCATION: (0)...(0)...
OTHER INFORMATION: Backbone is phosphorothioate--phosphodiester
OTHER INFORMATION: chimera
                                                                                                                                                                                 SUBLEMANT: Bavis, Heather L.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
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TITLE OF INVENTION: Therapeutic Protocols
CURRENT FILING DATE: 1998-05-20
PRIOR FILING DATE: 1997-05-20
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                                                              US-09-082-649B-58
Sequence 58, Application US/09082649B
Patent No. 6339068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-191-170-97

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) OTHER INFORMATION: Synthetic Oligonucleotide US-09-337-619-10
                                                                                                         US-09-692-170C-42

) Sequence 42, Application US/09692170C

: Patent No. 6562345
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Patent No. 6653292
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                                                                                                                                                      Patent No. 6562345
GENERAL INFORMATION:
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LENGTH: 20
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CTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising

OTHER INFORMATION: one or more CpG motifs
US-09-301-829A-1
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Query Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 1; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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100.0%; Score 20; DB 3;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                  Sequence 1, Application US/0969021
; Sequence 1, Application US/0969021
; Patent No. 6544518
; GRMERAL INFORMATION:
    APPLICANT: Friede, Martin
    APPLICANT: Friede, Martin
    APPLICANT: Hermand, Philippe
    TITLE OF INVENTION: Vaccines
    FILE REFERENCE: B45181-1
    CURRENT APPLICATION NUMBER: US/09/690,921
    CURRENT PILING DATE: 2000-10-18
    PRIOR APPLICATION NUMBER: 09/301,829
    PRIOR PILING DATE: 1999-04-29
    PRIOR APPLICATION NUMBER: 9908885.8
    PRIOR APPLICATION NUMBER: 990885.8
    PRIOR APPLICATION NUMBER: 990885.8
    PRIOR PILING DATE: 1999-04-19
    NUMBER OF SEQ ID NOS: 5
    MUMBER: FASELSEQ for Windows Version 3.0
    SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCORMATION:
APPLICANT: Friede, Martin
APPLICANT: Friede, Martin
TITLE OF INVENTION: VACCINES
FILE REPERENCE: B45181
CURRENT FLING DATE: 1999-04-29
FRIOR APPLICATION NUMBER: US/09/301,829A
CURRENT FILING DATE: 1999-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09301829A Patent No. 6558670
                                                                                      1 TCCATGACGTTCCTGACGTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0
Matches 20; Conservative

; TYPE: DNA
; ORGANISM: Human
US-09-690-921-1
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US-09-301-829A-1
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US-09-690-921-1
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| GENERAL INFORMATION:
| JAPLICANT: Diamond, Don J. |
| TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS |
| TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS |
| FILE REPRENDENCE: 1954-346 |
| CURRENT APPLICATION NUMBER: US 09/692,170C |
| PRIOR APPLICATION NUMBER: US 09/075,257 |
| PRIOR PILING DATE: 1998-02-10 |
| PRIOR PILING DATE: 1998-02-10 |
| PRIOR PILING DATE: 1998-02-10 |
| PRIOR PILING DATE: 1998-02-10 |
| PRIOR PILING DATE: 1996-11-12 |
| PRIOR PILING DATE: 1996-11-12 |
| NUMBER OF SEQ ID NOS: 44 |
| SOFTWARE: PARENTIN VERSION 3.1 |
| SEQ ID NO 42 |
| LEMENTING DATE: 200-11-12 |
| LEMENTING DATE: 1996-11-12 |
| SEQ ID NO 42 |
| LEMENTING DATE: 1997-11-12 |
| LEMENTING DATE: 1996-11-12 |
| LEMENTING DATE: 1996-11-12 |
| SEQ ID NO 42 |
| LEMENTING DATE: 1996-11-12 |
| LEMENTING DATE: 1996-11-12 |
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
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GENERAL INTORNATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Methods of Treating Cancer Using
TITLE OF INVENTION: Immunostimulatory Oligonucleotides
FILE REFERENCE: C1039/7021/HCL
CURRENT APPLICATION NUMBER: US/08/337,619
CURRENT APPLICATION NUMBER: US/08/337,619
EARLIER APPLICATION NUMBER: US 08/960,774
EARLIER APPLICATION NUMBER: US 08/738,652
EARLIER APPLICATION NUMBER: US 08/38,652
EARLIER APPLICATION NUMBER: US 08/38,603
EARLIER APPLICATION NUMBER: US 08/38,652
EARLIER APPLICATION NUMBER: US 08/38,663
EARLIER APPLICATION NUMBER: US 08/36,063
EARLIER APPLICATION NUMBER: US 08/276,358
EARLIER APPLICATION NUMBER: US 08/276,358
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COTHER INFORMATION: Synthetic DNA adjuvant
US-09-692-170C-42
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SOFTWARE: FastSEQ for Windows Version 3.0
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RESOURT NO. 673973

Sequence 42 Application US/09984365

Sequence 42 Application US/09984365

Patent No. 673973

FRICAL INFORMATION:

APPLICANT: Diamond, Don J

TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS

TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS

FILE REFERENCE: 1954-384

CURRENT FILING DATE: 2002-33-13

FRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 1090-02-10

PRIOR PLILING DATE: 1998-05-11

PRIOR PLILING DATE: 1998-05-11

PRIOR PLILING DATE: 1998-02-10

PRIOR PPLICATION NUMBER: US 09/051298

PRIOR PLILING DATE: 1998-02-10

PRIOR PPLICATION NUMBER: US 08/950064

PRIOR PLILING DATE: 1998-02-10

PRIOR PLILING DATE: 1998-02-10

PRIOR PLILING DATE: 1998-1-1-12

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.1

LENGTH: 20
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US-09-565-906-1
I US-09-565-906-1
| Sequence 1, Application US/09565906
| Patent NO. 6737066
| GENERAL INFORMATION:
| APPLICANT: MOSS, Ronald B. TITLE OF INVENTION: HIV Immunogenic Compositions and Methods:
| TITLE OF INVENTION: P-IM 4029
| CURRENT APPLICATION NUMBER: US/09/565,906
| CURRENT PILING DATE: 2000-05-05
| PRIOR APPLICATION NUMBER: US 60/132,762
| PRIOR APPLICATION NUMBER: US 60/150,667
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                      y Match 100.0%; Score 20; DB Local Similarity 100.0%; Pred. No. 1; neg 20; Conservative 0; Mismatches
                                                                                                                                                                                                 , OTHER INFORMATION: Synthetic DNA adjuvant US-10-238-607-42
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 20
                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
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Matches 20
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APPLICANT: Diamond, Don J.

TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
FILTE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
FILTE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
FILTE OF TRILING DATE: 2003-04-03
FRIOR PELING DATE: 2000-10-20
FRIOR PELING DATE: 2000-03-27
FRIOR APPLICATION NUMBER: US 09/031,298
FRIOR FILING DATE: 1998-05-11
FRIOR FILING DATE: 1998-02-10
FRIOR FILING DATE: 1998-02-10
FRIOR FILING DATE: 1999-10-14
FRIOR FILING DATE: 1999-10-14
FRIOR FILING DATE: 1996-11-12
FRIOR FILING DATE: 1996-11-12
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| Patent No. 6727093
| Patent No. 6727093
| GENERAL INFORMATION:
| APPLICATION:
| APPLICATION:
| APPLICATION: HCMV- REACTIVE T CELLS AND USES THEREFOR TILE REFRENCE: 1954-398
| CURRENT APPLICATION NUMBER: US/10/238,607
| CURRENT APPLICATION NUMBER: US/09/692,170
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-03-27
| PRIOR FILING DATE: 1998-02-10
| PRIOR FILING DATE: 1998-02-11
| PRIOR FILING DATE: 1998-02-11
| PRIOR FILING DATE: 1998-02-11
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| PRIOR FILING DATE: 1998-02-10
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| PRIOR FILING DATE: 1998-11-12
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                                            Query Match
100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 1;
Conservative 0; Mismatches n.
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/10405231A
Patent No. 6726910
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ORGANISM: Artificial sequence
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Matches 20; Conserve
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Sequence 56, Application US/09965101

Sequence 56, Application US/09965101

GENERAL INFORMATION:

APPLICANT: Davis, Heather L.

APPLICANT: Schorr, Joachim

APPLICANT: Schorr, Joachim

APPLICANT: W., Tong

TITLE OF INVENTION: Therapeutic Protocols

TITLE OF INVENTION: Therapeutic Protocols

TITLE OF INVENTION: Therapeutic Protocols

FILE REPERRECE: C1039/7057 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/965,101

CURRENT PILING DATE: 2001-09-26

PRIOR PPLING DATE: 1998-05-20

PRIOR APPLICATION NUMBER: US 60/047,233

PRIOR APPLICATION NUMBER: US 60/047,209

PRIOR APPLICATION NUMBER: US 60/047,209

PRIOR PRING DATE: 1997-05-20

NUMBER OF SEQ ID NOS: 84

SEQ ID NO 56

LENGTH: 20

MATHER OF SEQ ID NOS: 84

LENGTH: 20
TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Therapeutic Protocols; FILE REFERENCE: C1039/7057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/965,101
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/082,649
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 84
SOFFWARE: FRASEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic oligonucleotide MAMB/KRY: misc. feature LOCAFINS: (0): (0) OTHER INFORMATION: Has a phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic oligonucleotide
NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: Has phosphodiester backbone.
US-09-965-101-56
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.0%;
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 51
LENGTH: 20
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APPLICANT: Glenn, Gregory M.
APPLICANT: Glenn, Gregory M.
APPLICANT: Glenn, Gregory M.
TITLE OF INVENTION: Use of Penetration Enhancers and Barrier Disruption Agents to
TITLE OF INVENTION: Enhance the Transcutaneous Immune Response
FILE REPERRENCE: 4057-25
CURRENT APPLICATION NUMBER: US/09/257,188A
CURRENT PILING DATE: 1999-02-25
FRIOR PELING DATE: 1996-11-14
PRIOR PILING DATE: 1997-07-17
PRIOR PILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: US 60/075,850
PRIOR PILING DATE: 1999-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: US 60/086,251
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
ENGRETAL 20
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                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: phosphorothioate-modified synthetic
OTHER INFORMATION: oligodeoxynucleotide
                                                                                                                                                                                                                                                                                              Score 20; DB 3;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 20; DB 3; Best Local Similarity 100.0%; Pred. No. 1; Matches 20; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-257-188A-2
                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1; Matches 20; Conservative 0; Mismatches
  PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 20
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US-09-965-101-51
'Sequence 51, Application US/09965101
'Patent No. 6821957
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Patent No. 6797276
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GENERAL INFORMATION:
APPLICANT: ZEON CORPORATION
APPLICANT: ZEON CORPORATION
TITLE OF INVENTION: 6924135e1 DNA encoding Eimeria glyceroaldehyde-3-phosphate
TITLE OF INVENTION: dehydrogenase and uses thereof
FILE REFERENCE: GAPDH gene of Eimeria
CURRENT APPLICATION NUMBER: US/10/651,013
CURRENT PILLING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 14
SOCTHARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 20
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Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: Oligonuclectide
US-10-651-013-14
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Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0.
CRGANISM: Artificial sequence
FEATURE:
CTHER INFORMATION: Synthetic DNA adjuvant
US-10-697-055-42
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; OTHER INFORMATION: CpG nucleotides
US-09-917-2228-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/10651013
Patent No. 6924135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCATGACGITCCTGACGIT 20
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APPLICANT: Diamond, Don J.

APPLICANT: Diamond, Don J.

TITLE OF INVENTION: HGWV- REACTIVE T CELLS AND USES THEREFOR FILE REPRENEUE: 1954-1968

CURRENT APPLICATION NUMBER: US/10/697,055

CURRENT FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: US/09/692,170

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 1998-05-11

PRIOR APPLICATION NUMBER: US 09/075,257

PRIOR PILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-01-14

PRIOR FILING DATE: 1998-10-14

PRIOR FILING DATE: 1998-10-14

PRIOR FILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VERSE: US 08/747,488

PRIOR FILING DATE: 1996-11-12

NUMBER OF SEQ ID NOS: 43

LENGTH: 20
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NAME/KEY: misc_feature
| LOCATION: (0) ... (0)
| COTHER INFORMATION: Backbone is phosphorothioate--phosphodiester
| OTHER INFORMATION: chimera
| US-09-965-101-58
                                                                                                                                     US-US-US-19101-SE
Sequence 58, Application US/09955101
Patent No. 6821957
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Wu. Tong
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039/7057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/965,101
CURRENT FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 60/047,203
PRIOR APPLICATION NUMBER: US 60/047,203
PRIOR APPLICATION NUMBER: US 60/047,203
PRIOR APPLICATION NUMBER: US 60/047,203
PRIOR APPLICATION NUMBER: US 60/047,203
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PRIOR APPLICATION NUMBER: US 60/047,203
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels
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Patent No. 6843992
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ORGANISM: Artificial Sequence
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US-10-697-055-42
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US-09-965-101-58
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Search completed: December 30, 2005, 18:56:48 Job time : 98 secs
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US-09-554-987B-83
US-09-554-987B-83
US-09-554-987B-83

| Sequence 83, Application US/09554987B
| Patent No. 6943240
| GENERAL INFORMATION:
| APPLICANT: Stefan Bauer
| APPLICANT: Grayson B. Lipford
| APPLICANT: Hermann Wagner
| TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
| TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
| TITLE OF INVENTION: DATES FOR HIGH THROUGHPUT SCREENING OF
| TITLE OF INVENTION: DATES: 2001-09-17
| FILE REFERENCE: C1041/7016 (AWS)
| CURRENT FILING DATE: 2001-09-17
| PRIOR APPLICATION NUMBER: US 60/283,657
| PRIOR FILING DATE: 2001-01-23
| PRIOR FILING DATE: 2001-01-23
| PRIOR PELICATION NUMBER: US 60/283,657
| PRIOR PELING DATE: 2001-06-22
| NUMBER OF SEQ ID NOS: 230
| SOFTWARE: FeatSEQ for Windows Version 3.0
| SEQ ID NO 83
| LEMETH: 2001-06-22
| WARDER OF SEQ ID NOS: 230
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APPLICANT: Brainer, Robert L.
APPLICANT: Krieg, Arthur
ITILE OF INVENTION: Methods Related to Immunostimulatory
ITILE OF INVENTION: Methods Related to Immunostimulatory
ITILE OF INVENTION: Methods Related to Immunostimulatory
ITILE OF INVENTION: MOTORIER: US/09/672,126B
CURRENT PILING DATE: 1990-09-27
PRIOR APPLICATION NUMBER: 60/156,147
PRIOR PILING DATE: 1990-09-29
NUMBER OF SEQ ID NOS: 169
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
PRATURE:
PRATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-83
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; Sequence 83, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
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0; Mismatches
                  1 TCCATGACGTTCCTGACGTT 20
                                    1 rccardacerrccrdacerr 20
20; Conservative
Matches
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December 30, 2005, 18:49:36; Search time 494 Seconds (without alignments) 334.793 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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Maximum DB 8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Published Applications NA Main:*

1: /cgm2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgm2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
3: /cgm2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
4: /cgm2 6/ptodata/1/pubpna/USO8B_PUBCOMB.seq:*
5: /cgm2 6/ptodata/1/pubpna/USO8B_PUBCOMB.seq:*
6: /cgm2 6/ptodata/1/pubpna/USO8B_PUBCOMB.seq:*
7: /cgm2 6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
8: /cgm2 6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgm2 6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgm2 6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
10: /cgm2 6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-824-468-105 US-09-949-194-1 US-09-910-26A-86 US-09-800-26A-90 US-09-800-26A-90 US-09-950-013-86 US-09-920-313-86 US-09-920-313-86 US-09-920-313-86 US-09-920-313-86 US-09-920-313-86 US-09-920-313-86 US-09-913-888-326-562 US-09-888-326-563 US-09-776-479-153 US-09-776-479-223 SUMMARIES Query Match Length Score 221098765 221098765 2310876 Result

1, Appli 1, Appli 1, Appli 90, Appl 90, Appl 90, Appl 16, Appl 61, App 62, App 63, App

Sequence

3302 99480, 99480, 99551, 10023, 10028, 10028, 10028, 10023, 1003, 1003, 1003, 1003,	Sequence 223, App Sequence 302, App
US-09-776-479-302 US-09-776-479-948 US-09-776-479-949 US-09-776-479-951 US-09-776-479-951 US-09-776-479-952 US-09-776-479-953 US-09-776-479-953 US-09-776-479-954 US-09-776-479-958 US-09-776-479-958 US-09-776-479-958 US-09-776-479-958 US-09-776-479-958 US-09-776-479-958 US-09-776-479-958 US-09-776-479-137 US-09-984-366-42 US-09-776-479-137 US-09-776-479-137 US-09-776-479-137 US-09-776-479-137 US-09-776-479-137 US-09-776-479-137	US-09-776-479-223 US-09-776-479-302
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ALIGNMENTS

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TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of CpG and
TITLE OF INVENTION: Saponin and Methods Thereof
TITLE OF INVENTION: Saponin and Methods Thereof
TITLE OF INVENTION: Saponin and Methods Thereof
FILE REFERENCE: 8449-153-999
CURRENT PILING DATE: 2002-01-12
PRIOR REPLICATION NUMBER: 60/200,853
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-01-13
PRIOR PILING DATE: 2000-01-13
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1998-08-10
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 20
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US-09-760-506-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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US-09-768-012-3
is Sequence 3, Application US/09768012
j Patent No. US2001004416A1
j GENERAL INFORMATION:
j APPLICANT: Davis, Heather L.
j APPLICANT: McCluske, Michael J.
j TITLE OF INVENTION: Immunostimulatory Nucleic Acids for
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Pred. No. 5.6;
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                  Sequence 3, Application US/09760506
Publication No. US20010034330A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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US-09-760-506-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and TITLE OF INVENTION: Cytokines FILE REPERENCE: CURRENT PAPTICATION NUMBER: US/09/824,468
CURRENT FILING DATE: US/09/0286,098
PRIOR APPLICATION NUMBER: 09/286,098
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 105
LENGTH: 20
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TITLE OF INVENTION: VACCINES FOR BROAD SPECTRUM PROTECTION
TITLE OF INVENTION: AAINST DISEASES CAUSED BY NEISSERIA MENINGITIDIS
TITLE REFERENCE: CHORO1
CURRENT APPLICATION NUMBER: US/09/917,222
CURRENT FILING DATE: 2001-07-27
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APPLICANT: BEATZIET.
APPLICANT: PETATENDE.
TITLE OF INVENTION: Nucleic Acids for the Prevention and
TITLE OF INVENTION: Treatment of Sexually Transmitted Diseases
TITLE OF INVENTION: Treatment of Sexually Transmitted Diseases
TITLE OF INVENTION: Treatment of Sexually Transmitted Diseases
TITLE OF INVENTION: Treatment of Sexually Transmitted Diseases
FILE REFERENCE: C1037/7021 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/949,194
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/230,637
PRIOR APPLICATION NUMBER: US 60/230,637
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Synthetic Sequence US-09-949-194-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Sequence US-09-824-468-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-917-222-1
Sequence 1, Application US/09917222
Sequence No. US20020110569A1
Patent No. US20020110569A1
SENERAL INPORMATION:
APPLICANT: Granoff, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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i Sequence 100, Application US/09824468

i Sequence 100, Application US/09824468

i Sequence 100, Application US/0982468

i Patent No. US20020064515A1

i APPLICANT: Welner, George

i TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and

i TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and

i TITLE OF INVENTION: Temmene System Using Immunotherapeutic Oligonucleotides and

i TITLE OF INVENTION: Temmene System Using Immunotherapeutic Oligonucleotides and

i TITLE OF INVENTION: UNMER: US/09/824,468

i TITLE OF INVENTION NUMBER: US/09/824,468

FILE REFERENCE: C1039/7026/HCL

CURRENT APPLICATION NUMBER: US/286,098

PRIOR FILING DATE: 1999-04-02

NUMBER: OF SEQ ID NOS: 105

SEQ ID NO 100

LENGTH: 20

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; Sequence 105. Application US/09824468
patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%; Score 20; DB 3; Length 20; Local Similarity 100.0%; Pred. No. 5.6; Conservative 0; Minner.
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
                                     TITLE OF INVENTION: Inducing a Th2 Immune Response;
FILE REFERENCE: C1040/7010/HCL/MAT
CURRENT APPLICATION NUMBER: US/09/768,012
CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,461
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Synthetic Sequence
NAME/KEY: modified base
LOCATION: (8) ... (8)
COTHER INFORMATION: Cytosine is unmethylated.
NAME/KEY: modified base
LOCATION: (17) ... (17)
COTHER INFORMATION: Cytosine is unmethylated.
UCATION: (17) ... (17)
CHER INFORMATION: Cytosine is unmethylated.
US-09-768-012-3
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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LENGTH: 20
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; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Brateler, Robert L.
; APPLICANT: Bretersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of;
; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of;
; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of;
; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of;
; CURRENT APPLICATION NUMBER: US/09/800,266A
; CURRENT FILING DATE: 2000-03-03
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 146
; SOUTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 20
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APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TURERY FILING DATE: 2001-03-05
FRIOR PILING DATE: 2001-03-05
FRIOR PILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 146
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
LENGTH: 20
TYPE: DNA
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Best Local Similarity 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0. 77471
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5.6;
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 20; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90, Application US/09800266A Patent No. US20020156033A1 GENERAL INFORMATION:
                                                                                                                                                                                        ) OTHER INFORMATION: CpG nucleotides US-09-917-222-1
                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCCATGACGTTCCTGACGTT 20
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                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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US-09-800-266A-86
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US-09-895-007A-86

US-09-895-007A-86

Sequence 86, Application US/09895007A

Patent No. US20020165178A1

GENERAL INPORMATION:

APPLICANT: Schetter, Christian

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE

TITLE OF INVENTION: TREATMENT OF ANEMIA, THROMBOCTTOPENIA,

FILE REFERENCE: C1041/7014 (AWS)

CURRENT FILING DATE: 2001-06-28

PRIOR FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 133

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 86

LENGTH: 20

TENGTH: 20

TENGTH: 20

TENGTH: 20

TENGTH: 20

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US-09-895-007A-90

i Sequence 90, Application US/09895007A

patent No. US20020165178A1

i GENERAL INFORMATION:

APPLICANT: Schetter, Christian

APPLICANT: Bratzler, Robert L.

APPLICANT: Bratzler, Robert L.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE

TITLE OF INVENTION: TREATMENT OF ANEMIA, THROMBOCYTOPENIA,

FILE REFERENCE: C1041/7014 (AMS)

CURRENT APPLICATION NUMBER: US 60/214,368

PRIOR FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 133

SOUTH NUMBER OF SEQ ID NOS: 133

SOUTH NUMBER OF SEQ ID NOS: 133

SOUTH NUMBER OF SEQ ID Windows Version 3.0
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Pred. No. 5.6;
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; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-90
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                                                                                                      Query Match
100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 20; Conservative 0; Mismatches
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; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-90
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Matches 20; Conservative
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sequence 561, Application US/09888326
sequence 561, Application US/09888326
sequence 561, Application US/09888326
sequence 561, Application No. US20030026801A1
sexpection No. US20030026801A1
sexpection No. US20030026801A1
sexpection No. Genther
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION UNMERS: US 60/213,346
sexpection No. Sexpection No. Sexpection 3.0
sexpection No. Sexpection No. Sexpection 3.0
sexpection No. Sexpection No. Sexpection 3.0
sexpection No. Sexpection No. Sexpection 3.0
                                                                         Sequence 560, Application US/0988326
; Publication No. US2030026801A1
; GENERAL INFORMATION:
    APPLICANT: Weiner, George
; APPLICANT: Hartwann, Gunther
    TITLE OF INVENTION: Cell Lysis and Treating Cancer
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REPERENCE: Class; (AMS)
; CURRENT APPLICATION UNDER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION UNDERER: US 60/213,346
; PRIOR PILING DATE: 2000-06-22
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; OTHER INFORMATION: Synthetic oligonucleotide
US-09-888-326-561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic oligonucleotide NAME/KEY: misc feature LOCATION: (0)...(0) OTHER INFORMATION: phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 560
LENGTH: 20
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                 RESULT 13
US-09-888-326-560
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APPLICANT: Bratzler, Robert L.
APPLICANT: Petezsen, Deanna M.
TITLE OF INVENTION: Nucleic Acids for the Prevention and
TITLE OF INVENTION: Treatment of Gastric Ulcers
TITLE OF INVENTION: Treatment of Gastric Ulcers
FILE REPRENCE: C1037/7019 (HCL/MAT)
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 60/222,248
PRIOR APPLICATION NUMBER: US 60/222,248
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PRACES OF WINDOWS VERSION 3.0
SEQ ID NO 90
SEQ ID NO 90
LENGTH: 20
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Sequence 86, Application US/09920313
; Sequence 86, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
   APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Treatment of Gastric Ulcers
   TITLE OF INVENTION: Treatment of Gastric Ulcers
; TITLE REFERENCE: 1033/7019 (HCL/MAT)
; CURRENT PILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR PILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTHARE: PRACESQ for Windows Version 3.0
; SEQ ID NO 86
; SEQ ID NO 86
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Query Match
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-90
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; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-86
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; Sequence 90, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 20; Conserv
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OTHER INFORMATION: Synthetic oligonucleotide

NAME/KEX: misc_feature

LOCATION: (0)...(0)

OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone

OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
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; Sequence 562, Application US/0988326; Publication No. US20030026801A1
; GENERAL INPOWATION:
; APPLICANT: Weiner, George; TILL OF INVENTION: GENERAL ENDOMOTION:
; TILL OF INVENTION: Methods for Enhancing Antibody-Induced; TILLE OF INVENTION: Methods for Enhancing Antibody-Induced; TILLE REFERENCE: C10139/7052 (AWS); CURRENT APPLICATION NUMBER: US/09/888,326; CURRENT FILING DATE: 2001-06-22; PRIOR FILING DATE: 2001-06-22; PRIOR FILING DATE: 2000-06-22; NUMBER: OF SEQ ID NOS: 848; SOFTWARE: PastSEQ for Windows Version 3.0; SEQ ID NO 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 563, Application US/0988326
Fublication No. US20030026801A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Methods for Enhancing Cancer
TITLE OF INVENTION: George
TITLE OF INVENTION: George
FILE REFERENCE: C1039/7052 (AMS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR PLLING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 563
LENGTH: 20
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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| Sequence 47, Application US/09931583
| Publication No. 20030050263A1
| GENERAL INFORMATION:
| APPLICANT: Krieg, Arthur
| APPLICANT: Klimman, Dennis
| APPLICANT: Klimman, Dennis
| APPLICANT: Steinberg Alfred
| TITLE OF INVENTION: Methods and Products for Treating HIV Infection
| FILE REFERENCE: C1039/7053 (HCL)
| CURRENT PELLING DATE: 2001-08-16
| PRIOR APPLICATION NUMBER: US 08/276,358
| PRIOR APPLICATION NUMBER: US 09/415,142
| PRIOR APPLICATION NUMBER: US 09/415,142
| PRIOR APPLICATION NUMBER: US 09/415,142
| PRIOR APPLICATION NUMBER: US 09/415,142
| PRIOR APPLICATION NUMBER: US 09/415,142
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| PRIOR APPLICATION NUMBER: US 09/415,142
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| PRIOR APPLICATION NUMBER: US 09/415,142
| PRIOR APPLICATION NUMBER: US 09/415,142
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                                                                                                          APPLICANT: Kline, Joel N.
APPLICANT: Kline, Joel N.
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
FILE REPERANT: Seliberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7048 (AMS)
CURRENT APPLICATION NUMBER: US/09/818,918
CURRENT FILING DATE: 1994-07-15
FRIOR APPLICATION NUMBER: US 08/276,358
FRIOR APPLICATION NUMBER: US 08/36,063
FRIOR PILING DATE: 1995-02-07
FRIOR FILING DATE: 1995-02-07
FRIOR APPLICATION NUMBER: US 08/738,652
FRIOR APPLICATION NUMBER: US 08/738,652
FRIOR PILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 20
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100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic Oligonucleotide
US-09-931-583-47
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Sequence 10, Application US/09818918
Publication No. US20030050261A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                APPLICANT: Krieg, Arthur M
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Best Local Similarity 100.
Matches 20; Conservative
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RESULT 19

RESULT 17 US-09-818-918-10

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Query Match
Best Local Similarity
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Sequence 137, Application US/09776479

PUBLIcation No. US20030087848A1

PUBLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Fouron, Yeve

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

TITLE OF INVENTION: Treatment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 60/179,991

PRIOR PILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SEQ ID NO 137

LENGTH: 20

LENGTH: 20
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                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT)

FILE REFERENCE: C1037/7013 (HCL/MAT)

FILE REFERENCE: C1037/7013 (HCL/MAT)

FILE REPERENCE: C1037/7013 (HCL/MAT)

FILE REPERENCE: C1037/7013 (HCL/MAT)

FILENGTH: 2001-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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         Sequence 69, Application US/09776479
Publication No. US20030087848A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 20; Conservative
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US-09-776-479-137
US-09-776-479-69
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; Sequence 113, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INPORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: IMMUNOSTIMULATOR (URLANT)
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
; SEQ ID NO 153
; LENGTH: 20
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APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Immunostimulatory Nucleic Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
RAIOR FILING DATE: 2000-00-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 20
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Sequence 223, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Pouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
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; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-153
                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-152
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 20; Conservative
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RESULT 26
US-09-776-479-949
; Sequence 949, Application US/09776479
; Sequence 949, Application WS/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Aethma and Allergy
; FILE REFERENCE: Closty77013 (HCL/MAY)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT PILING DATE: 2001-02-02
; PRIOR PILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
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                SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                             ) OTHER INFORMATION: Synthetic Sequence US-09-776-479-948
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                                                                                                                                                                                                                                                                                                     1 TCCATGACGITCCTGACGIT 20
                                                                                                                                                                                                                                                                                                                                 1 TCCATGACGTTCCTGACGTT 20
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                                                                                                   ORGANISM: Artificial Sequence
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                                  SEQ ID NO 948
LENGTH: 20
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LENGTH: 20
                                                                                TYPE: DNA
                                                                                                                          FEATURE:
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US-09-776-479-302
US-09-776-479-302
Sequence 302, Application US/09776479
Fublication No. US20030087848A1
GENERAL INFORMATION:
JAPPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Pouron, Yves
JITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION INPERS: US/09/776,479
CURRENT FILING DATE: 2000-02-03
FRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 302
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 948, Application US/09776479
Fublication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
FRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: RASISEQ for Windows Version 3.0
LENGTH: 20
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OTHER INFORMATION: Synthetic Sequence
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                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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US-09-776-479-948
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unery Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 20; Conservative 0; Mismatches 0; Tindel
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Sequence 952, Application US/09776479

Publication No. US20030087848A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Pouron, Yves

TITLE OF INVENITON: Immunostimulatory Nucleic Acids for the TITLE OF INVENITON: Immunostimulatory Nucleic Acids for the TITLE OF INVENITON: Treatment of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT)

FILE REFERENCE: C1037/7013 (HCL/MAT)

FILE REFERENCE: C1037/7013 (HCL/MAT)

FILE REFERENCE: C1037/7013 (HCL/MAT)

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FILE REFERENCE: C1037/7013 (HCL/MAT)
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; Sequence 951, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Bretzen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT)
; TITLE OF INVENTION: Treatment of Asthma and Allergy FILE REFERENCE: 2001-02-02
; RIGHT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 5.6; tive 0; Mismatches 0; Indels
                                                                                                                                  100.0%; Score 20; DB 3; Length 20; illarity 100.0%; Pred. No. 5.6; Conservative 0; Mismatches 0; Indels
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SOCHWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 951
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Sequence US-09-776-479-951
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-950
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 20, Conservative
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
US-09-776-479-951
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100.0%; Score 20; DB 3; Length 20;

US-09-776-479-952

Query Match

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            0; Indels
100.0%; Pred. No. 5.6;
tive 0; Mismatches
  Best Local Similarity 100. Matches 20; Conservative
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APPLICANT: Breazler, Robert L.
APPLICANT: Breazler, Deanna M.
APPLICANT: Petersen. Deanna M.
APPLICANT: Petersen. Deanna M.
APPLICANT: Petersen. Deanna M.
APPLICANT: Petersen. Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: WHERE: US/09/776,479
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
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US-09-776-479-953
Sequence 953, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
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